T95 19

#### STIC-Biotech/ChemLib

From:

Slobodyansky, Elizabeth

Sent:

Monday, September 13, 1999 5:22 PM

To:

STIC-Biotech/ChemLib

Subject:

09/068,507

This is a date case, please let me know if I need to do anything to facilitate.

Please search for case 09/068,507:

1. Seq ID NOs 1 + 2 against commercial and interference databases.

Thank you very much.

Elizabeth Slobodyansky





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#### IMPORTANT INFORMATION ABOUT YOUR SEQUENCE SEARCH:

#### Compugen Sequence searching hardware and software explained:

This is the new sequence searching system that is currently being phased into as a replacement for the Maspar/Mpsrch platform. This system has been tested by both searchers and examiners, and has shown equivalent results to the Maspar system for the same databases. The results output format for all Compugen printed results are essentially the same except for translations.

#### Translation searching on Compugen explained:

The Compugen system utilizes Framesearch software for translations of proteins to nucleotides, and nucleotides to proteins. Some examiners have found these to be superior to the backtranslate software on Maspars.

FrameSearch searches a group of protein sequences for similarity to one or more nucleotide query sequences, or searches a group of nucleotide sequences for similarity to one or more protein query sequences. For each sequence comparison, the program finds an optimal alignment between the protein sequence and the corresponding codons on each the nucleotide sequence. Optimal alignments may include reading frame shifts. Please see any of the professional searching staff if you need assistance with this format.

#### File extensions for Compugen results transferred to floppy disks.

Compugen system search results will be delivered in one of two possible formats:

- 1. Standard concatenated files with .flp extension.
- Compressed .zip files which decompressed yield two files as described below:

US08123456.cmr - Contains all commercial databases, may include Issued
US08123456.pen - Contains pending file results only

#### VERY IMPORTANT NOTE ABOUT PENDING FILE SEARCHES.

If your search contains file names with the following bolded extensions:

US08123456.rap US08123456.rnp

Do not leave this search in the case, during prosecution, or after the case issues, since it contains pending data which is confidential.

#### QUESTIONS? Contact any of the following:

Dilip Pandya, Chief, Information Branch, 308-4268

#### Professional searching staff:

John Dantzman (308-4488); Jan Delaval (308-4498); Mary Hale (308-4258); Barb O'Bryen (308-4291); David Schreiber (308-4292); Paula Sheppard (308-4499); Mark Spencer (308-4266); Beverly Shears (308-4994); Alex Waclawiw (308-4491).

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1.1		

### FOR OFFICIAL USE ONLY 195-19 U.S. DEPARTMENT OF COMMERCE Patent and Trademark Office SEARCH REQUEST FORM Examiner # (Mandatory): Requester's Full Name: Art Unit \_\_\_\_\_ Location (Bldg/Room#): \_\_\_\_\_/OD//\_ Phone (circle 305 306 308) \_\_ Serial Number: \_\_\_ Results Format Preferred (circle): PAPER DISK E-MAIL Title of Invention Inventors (please provide full names): Earliest Priority Date: Keywords (include any known synonyms registry numbers, explanation of initialisms): Search Topic: Please write detailed statement of the search topic, and the concept of the invention. Describe as specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples of relevant citations, authors, etc., if known. You may include a copy of the abstract and the broadcast or most relevant claim(s). FOR OFFICIAL USE ONLY STAFF USE ONLY Searcher: BOB Type of Search Vendors (include cost where applicable)

\_\_/\_ N.A. Sequence

\_ A.A. Sequence

\_ Structure (#)

\_ Bibliographic

Litigation1

Procurement

Fulltext

\_ Other

Searcher Location:

Date Picked Up:

Date Completed :\_

Clerical Prep Time:

Number of Databases:\_

Terminal Time:

PTO-1590 (2-99)

STN

\_ Dialog

Dr. Link

Westlaw Other (specify)

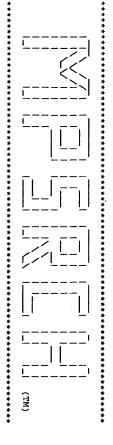
\_\_ Questel/Orbit

Lexis/Nexis

\_\_ WWW/Internet

MP 2 In-house sequence systems (list)

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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Wed Sep 15 10:37:50 1999; MasPar time 11.18 Seconds 49.467 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: >US-09-068-507A-1 (1-26) from US09068507A.pep 199

Sequence: 1 KSSAYSLOMGATAIKQVKKLFKKWGW 26

Scoring table:

PAM 150 Gap 15

Searched: 170751 seqs, 21266608 residues

Post processing: Minimum Match 0% Listing first 45 summaries

Database:

a-geneseq35
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29 30:part30 31:part31 32:part32 33:part33
34:part34 35:part35 36:part36 37:part37 38:part38
39:part39

Statistics: Mean 22.683; Variance 77.937; scale 0.291

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Result	Score	ァィ	Length	D8	Ħ	Description	Pred. No.
<b>1</b>	199	100.0	26	24	W17989	Bacteriocin-inducing	2.87e-13
2	77	38.7	822	ü	W69847	Amino acid sequence o	4.40e+00
ω	75	37.7	793	29	W40117	Human GABA-BRla/b rec	6.84e+00
4	75	37.7	844	29	W40118	Rat GABA-BR1b recepto	6.84e+00
v	75	37.7	844	29	W40119	Human GABA-BR1b recep	6.84e+00
σ	75	37.7	960	29	W40116	Rat GABA-BRla recepto	6.84e+00
7	71	35.7	572	13	R78520	Partial ALK protein.	1.64e+01
8	67	33.7	234	34	W62742	Streptococcus pneumon	3.87e+01
9	64	32.2	115	<u>μ</u>	W28166	Staphylococcus aureus	7.28e+01
10	62	31.2	467	28	W41077	T. litoralis ADPHK pr	1.10e+02
11	62	31.2	572	æ	R39284	Parainfluenza virus t	1.10e+02
12	62	31.2	1577	16	R91047	Alpha-D-glucosyltrans	1.10e+02
13	60	30.2	13	24	W12897	Antimicrobial cationi	1.67e+02
14	60	30.2	74	18	R95262	Bacteriocin derivativ	1.67e+02
15	60	30.2	128	33	W61021	Streptococcus pneumon	1.67e+02
16	60	30.2	305	26	W23077	Sulfolobus solfataric	1.67e+02

⊬្រុ	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17
59	л U O U	59	59	59	59	59	59	59	59	59	59	59	59	59	59	59	59	59	59	59	59	60	60	60	60	60	60
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1462 7	797																										
7 R37508	W3650					8 R98132			R2402	R389	W3778	묫	R9811	89	R9811	R9812	Rg	묫	R9812	묫	R2255	R3195	P9480	R0602	P947	R790	
Human DNA polymerase	RENT1 F	u8 antigen.	Sequence encoded by L	•	Lymphocyte associated			mphocyte h	Sequence of human lym		Homo sapiens lymphocy	Human lymphocyte cell	lymphocyte			lymphocyte	lymphocyte	lymphocyte	lymphocyte	Human lymphocyte cell	cyte-spe	Sequence encoded by p	Parainfluenzae-3 gene	ᄄ	rain of tr	inin	Sequence of bovine pa
2.04e+02			•		•		•			, 6			2.04e+02				ŏ	ő	و	ő	ő	51	. 67	. 67	. 67	.67e+	

### ALIGNMENTS

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RESULT
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AC WA
DT 01
DE HA
KW GA
KW 11
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                                                                                                                                                                                                                                                                                                                                                 PT (disorders or tumours

PS (Claim 1d; Pages 107-109; 133p); English.

CC The present sequence represents a p96 protein. This protein is present

CC the secretion associated 17s (SA-17s) complex. Eight proteins form the

CS A-17s complex, which binds a syntaxin-containing (SC) complex. The

CC SA-17s complex, which binds a syntaxin-containing (SC) complex. The

CC SA-17s polypeptides and nucleotide sequences encoding them can be used

CC GA-17s polypeptides and nucleotide sequences encoding them can be used

CC synaptic transmission and other secretory processes. Compounds which

CC enhance binding between the SA-17s and SC complexes may be used to treat

CC anxiety disorders uch as depression, manic-depressive disorders and

CC anxiety disorders, or a neurodegenerative disease such as Parkinson's

CC disease or Huntington's disease. Compounds which inhibit binding between

CC disease or Huntington's disease. Compounds which inhibit binding between

CC such as schizophrenia, or for anaesthesia. The compounds can also be used

CC imbalances, the immune system for treatment of hormonal

CC imbalances, the immune system for intervention in antigen processing,

CC anti-tumour applications, such as regulation of membrane trafficking

CC during rapid cell division.
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Best Local :
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Human GABA-BRİa/b receptor protein.

Gamma-animobutyric acid; GABA-BRİa/b receptor; human; brain; agonist;
inhibitory neurotransmitter; peripheral nervous system; antagonist;
treatment; dementia; depression; anxiety; bronchial inflammation; ast
                                                                           W40117 standard; Protein; W40117; W40117; O3-JUN-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Amino acid sequence of p96, a protein present in SA-17S complex. p96 protein; secretion associated 17S complex; SA-17S; syntaxin-containing complex; SC complex; Screening; modulate; vesicular release; synaptic transmission; secretory process; treatment; affective disorder; depression; manic-depressive disorder; anxiety disorder; neurodegenerative disease; schizophrenia; anaesthesia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated vesicule secretion associated poly:peptide(s) develop products for treating e.g. effective disorder,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        neurodegenerative disease, hormone imbalances, immune system
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(STRD ) UNIV LELAND
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07-OCT-1998 (first entry)
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                                                                                                                 standard; Protein; 793
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Similarity 100.0%;
26; Conservation
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Pred. No.
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Pred. No. 2.87e-13;
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This sequence represents a novel rat GABA-B receptor protein, GABA-BRIb. GABA (gamma-aminobutyric acid) is the major inhibitory neurotransmitter found in the brain and peripheral nervous system and this receptor may be used for the identification of GABA-B receptor agonists and antagonists. Such proteins may be used in treatment of dementia, depression, anxiety, epilepsy, spasticity, bronchial inflammation or asthma or to improve cognitive function. GABA-B receptor ligands and probes derived from this sequence can be used to assay for GABA-B receptors or DNA encoding them.
            Matches
                                        Query Match
Best Local :
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Best Local Similarity
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This sequence represents a novel human GABA-B receptor protein, GABA-BRIA/b. GABA (gamma-aminobutyric acid) is the major inhibitory neurotransmitter found in the brain and peripheral nervous system and this receptor may be used for the identification of GABA-B receptor agonists and antagonists. Such proteins may be used in treatment of dementia, depression, anxiety, epilepsy, spasticity, bronchial inflammation or asthma or to improve cognitive function. GABA-B receptor ligands and probes derived from this sequence can be used to assay for GABA-B receptors or DNA encoding them.
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Bettler B, Bittiger H,
WPI; 98-042183/04.
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19-MAR-1997; E01370.
22-NOV-1996; US-756091.
30-MAY-1996; US-655716.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rat GABA-BR1b receptor protein.

Gamma-animobutyric acid; GABA-BR1b receptor; rat; brain; agonist; inhibitory neurotransmitter; peripheral nervous system; antagonist; treatment; dementia; depression; anxiety; bronchial inflammation; a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bettler WPI; 98-
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19-MAR-1997; E01370.
22-NOV-1996; US-756091.
30-MAY-1996; US-655716.
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WO9746675-A1.
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                                  Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cognitive function.
         37.7%;
larity 87.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Froestl W, Kaupmann K, Mickel
   Score 75;
Pred. No.
0; Misma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 75; DB 29; L
Pred. No. 6.84e+00;
0; Mismatches 1;
         Mismatches
; DB 29; Leu
. 6.84e+00;
. _ _ _ 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 793;
                                                              Length 844;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
         0;
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   Gaps
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19 KLFKKWGW 26

W40119 standard; Protein; 844 AA

03-JUN-1998 (first entry)

W40119;

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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              purified GABA-B receptor or receptor protein - and antagonists of these which may be useful in treating nervous system disorders Claim 4; Page 86-90; 108pp; English.

This sequence represents a novel human GABA-B receptor protein, GABA-BRID. GABA (gamma-aminobutyric acid) is the major inhibitory neurotransmitter found in the brain and peripheral nervous system and this receptor may be used for the identification of GABA-B receptor agonists and antagonists. Such proteins may be used in treatment of dementia, depression, anxlety, epilepsy, spasticity, bronchial inflammation or asthma or to improve cognitive function. GABA-B receptor ligands and probes derived from this sequence can used to assay for GABA-B receptors or DNA encoding them.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-DEC-1997.
19-MAR-1997; E01370.
19-MAR-1996; US-756091.
30-MAY-1996; US-655716.
(NOVS ) NOVARTIS AG.
Bettler B, Bittiger H, Froestl W, Kaupmann K, Mickel SJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human GABA-BRib receptor protein.

Gamma-animobutyric acid; GABA-BRia/b receptor; human; brain; agonist; inhibitory neurotransmitter; peripheral nervous system; antagonist; treatment; dementia; depression; anxiety; bronchial inflammation; asthma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 98-042183/04.
N-PSDB; V10267.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
WO9746675-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    epilepsy; cognitive function.
these which may be useful in treating nervous system disorders Claim 4; Page 50-56; 108pp; English.
This sequence represents a novel rat GABA-B receptor protein, GABA-BRIA. GABA (gamma-aminobutyric acid) is the major inhibitory neurotransmitter found in the brain and peripheral nervous system and this receptor may be used for the identification of GABA-B receptor agonists and antagonists. Such proteins may be used in treatment of dementia, depression, anxiety, epilepsy, spasticity,
                                                                                                                                                                                                                                                                                                                                                                           03-JUN-1998 (first entry)
Rat GABA-BRLA receptor protein.
Gamma-animobutyric acid; GABA-BRLA receptor; rat; brain; agonist;
inhibitory neurotransmitter; peripheral nervous system; antagonist;
treatment; dementia; depression; anxiety; bronchial inflammation; asthma;
                                                                                                                                                                                       (NOVS) NOVARTIS AG.
Bettler B, Bittiger H, Froestl W, Kaupmann K, Mickel WPI; 98-042183/04
                                                                                                                                                                                                                                              22-NOV-1996; US-756091.
30-MAY-1996; US-655716.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        w40116 standard; Protein; 960 AA.
w40116;
                                                                                                                                                                         N-PSDB; V10264.
                                                                                                                                                                                                                                                                                 11-DEC-1997.
19-MAR-1997; E01370.
                                                                                                                                                                                                                                                                                                                                                           epilepsy; cognitive function.
                                                                                                                                                    Purified GABA-B receptor or receptor protein - and antagonists
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         182 klfekwgw 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19 KLFKKWGW 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        844 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 75; DB 29;
Pred. No. 6.84e+00;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 844;
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        ID ACC PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; 03-5541.
N-PSDB; 03-5541.
N-PSDB; 03-5541.
N-PSDB; 03-541.
Methods for detecting human t(2;5) lymphoma - for detection and diagnosis of anaplastic large cell lymphoma(s) claim 21; Page 40-42; 70pp; English.
Claim 21; Page 40-42; 70pp; English.
The translocation event that occurs in human t(2;5) lymphoma that translocation event that occurs in human t(2;5) lymphoma of the translocation event that occurs in human t(2;5) lymphoma of the translocation event that occurs in human t(2;5) lymphoma of the translocation event that occurs in human t(2;5) lymphoma of the translocation event that occurs in human t(2;5) lymphoma of the translocation event that occurs in human t(2;5) lymphoma of the translocation event that occurs in human t(2;5) lymphoma of the translocation event that occurs in human t(2;5) lymphoma of the translocation event that occurs in human t(2;5) lymphoma of the translocation event that occurs in human t(2;5) lymphoma of the translocation event that occurs in human t(2;5) lymphoma of the translocation event that occurs in human t(2;5) lymphoma of the translocation event that occurs in human t(2;5) lymphoma of the translocation event that occurs in human t(2;5) lymphoma of the translocation event that occurs in human t(2;5) lymphoma of the translocation event that occurs in human t(2;5) lymphoma of the translocation event that occurs in human t(2;5) lymphoma of the translocation event that occurs in human t(2;5) lymphoma of the translocation event that occurs in human t(2;5) lymphoma of the translocation event that occurs in human t(2;5) lymphoma occurs in human t(2;5) lymphoma occurs in human t(2;5) lymphoma occurs in human t(2;5) lymphoma occurs in human t(2;5) lymphoma occurs in human t(2;5) lymphoma occurs in human t(2;5) lymphoma occurs in human t(2;5) lymphoma occurs in human t(2;5) lymphoma occurs in human t(2;5) lymphoma occurs in human t(2;5) lymphoma occurs in human t(2;5) lymphoma occurs in human t(2;5) lymphoma occurs in human t(2;5) lymphoma occurs in human t(2;5) lymphoma occurs 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-DEC-1994; U13947.
03-DEC-1993; US-160861.
(SJUD-) ST JUDE CHILDREN'S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALK protein; protein-tyrosine-kinase; fusion protein; NPM protein; nucleolar phosphoprotein; anaplastic large cell lymphoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R78520 standard; Protein; 572 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Look AT, Morris S
WPI; 95-215226/28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              t(2;5) translocation; diagnosis; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Partial ALK protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9515331-A.
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                                                                                                                                                                                                                                                                                                                04-JUN-1998.
24-NOV-1997; U21976.
27-NOV-1996; US-031879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptococcus pneumoniae polypeptide.
Polypeptide; ORF; open reading frame; infection; bacterial; streptococcal; bacteremia; diagnosis; prophylaxis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W62742 standard;
W62742;
09-NOV-1998 (fin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ribozymes.
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                                Streptococcus pneumoniae polynucleotides - useful for developing products for diagnosis, prevention and treatment of infections e
                                                                                                                   Reid RH, Zarfos PN WPI; 98-322654/28.
                                                                                                                                                        Black MT, Hodgson JE,
Reid RH, Zarfos PN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptococcus pneumoniae.
                                                                                                                                                                                                                                  (SMIK ) SMITHKLINE BEECHAM CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9823631-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19 KLFKKWGW 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              960 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            572 AA;
or diagnosis, prevention and treatment of bacteremia, meningitis or endocarditis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35.7%;
                                                                                                                                                                                         Knowles DJC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RES HOSPITAL
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 71; DB 13; Le
Pred. No. 1.64e+01;
""" matches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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                                                                                                                                                                                                     Lonetto MA, Nicholas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6.84e+00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence represents a Staphylococcus aureus protein of unknown function. The DNA sequence was isolated from a library of clones of S. aureus WCH 29 in Escherichia coli. The DNA sequence can be used in the construction of ribozymes and antisense sequences to control the expression of Staphylococcal genes. The DNA sequence is also useful as a source of regulatory elements for the control of bacterial gene expression. The present protein may be used to produce vaccines to enable a host to produce specific antibodies with a notit against invasion by S. aureus, and conditions relating to Staphylococcal infection, e.g. Staphylococcal food poisoning, scaled
                                                                         T. litoralis ADPHK protein sequence, SEQ ID NO 2.
ADPHK; enzyme; hexokinase; hexose 6-phosphate; adenosine 1-phosphate; adenosine 2-phosphate; hexose.
Thermococcus litoralis. J09327297-A.
                                                                                                                                                                                                                                                                                         W41077 standard; Protein; 467
                                                                                                                                                                                                                        05-MAY-1998
                                                                                                                                                                                                                                                                       W41077;
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19-FEB-1997; U02318.
20-FEB-1996; US-011888.
(SMIK ) SMITHKLINE BEECHAM CORP.
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Staphylococcus aureus protein; ribozyme; antisense sequence; control; Staphylococcal gene; regulatory element; bacterial gene expression; vaccine; Staphylococcal infection; food poisoning; scaled skin syndrometric staphylococcal infection; food poisoning; scaled skin syndrometric staphylococcal infection; food poisoning; scaled skin syndrometric staphylococcal infection; food poisoning; scaled skin syndrometric staphylococcal infection; food poisoning; scaled skin syndrometric staphylococcal surface protein; staphylococcal surface protein; staphylococcal surface protein; staphylococcal surface protein; staphylococcal surface protein; staphylococcal surface protein; staphylococcal surface protein; staphylococcal surface protein; staphylococcal surface protein; staphylococcal surface protein; staphylococcal surface protein; staphylococcal surface protein; staphylococcal surface protein; staphylococcal surface protein; staphylococcal surface protein; staphylococcal surface protein; staphylococcal surface protein; staphylococcal surface protein; staphylococcal surface protein; staphylococcal surface protein; staphylococcal surface protein; staphylococcal surface protein; staphylococcal surface protein; staphylococcal surface protein; staphylococcal surface protein; staphylococcal surface protein; staphylococcal surface protein; staphylococcal surface protein; staphylococcal surface protein; staphylococcal surface protein; staphylococcal surface protein; staphylococcal surface protein; staphylococcal surface protein; staphylococcal surface protein; staphylococcal surface protein; staphylococcal surface protein; staphylococcal surface protein; staphylococcal surface protein; staphylococcal surface protein; staphylococcal surface protein; staphylococcal surface protein; staphylococcal surface protein; staphylococcal surface protein; staphylococcal surface protein; staphylococcal surface protein; staphylococcal surface protein; staphylococcal surface protein; staphylo
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Claim 6; Page 507; 989pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel polypeptide(s) from Staphylococcus aureus strain WCUH29 - used to isolate antimicrobial compounds, and in vaccines against S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 97-424969/39.
N-PSDB; T84091.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 5; Page 32; 181pp; English.

The sequence is that of a Streptococcal polypeptide.

The polypeptide can potentially be used for the diagnosis and prevention of bacterial infections, especially Sp infection.

It may be used for the treatment of diseases such as otitis media, conjunctivitis, pneumonia, bacteremia, meningitis, sinusitis, pleural empyema, endocarditis or infection of the cerebrospinal fluid.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ome, and toxic shock syndrome.
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Pred. No. 7.28e+01;
6; Mismatches 7
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Pred. No. 3.87e+01;
5; Mismatches 6;
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scaled skin syndrome;
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N. P5DB; Q45684.

Multimeric hybrid genes and their chimeric proteins - are multimeric hybrid genes and their chimeric proteins e.g. Traccines against multiple pathogenic infections e.g. Traccines against with and respiratory syncytial virus can be seen and respiratory syncytial virus.

Claim 11; Figure 3A-3E; 80pp; English.

Character in the gene sequences which are linked and encode antigenic consists of two gene sequences which are linked and encode antigenic regions, these two sequences being derived from two different pathogens (parainfluenza virus (PIV) and respiratory syncitial virus CRSV). The gene sequences that are particularly used are those consists of two gene sequences that are particularly used are those consists of two gene sequences that are particularly used are those consists of two gene sequences that are particularly used are those consists of two gene sequences that are particularly used are those consists of two gene sequences that are particularly used are those consists of two genes sequences that are particularly used are those consists of two genes sequences that are particularly used are those consists of two genes sequences that are particularly used are those consists of two genes sequences and two genes sequences that are particularly used are those consists of two genes sequences that are particularly used are those consists of two genes are two genes and two genes are two genes and two genes are two genes as a vaccine. The gene gene genes are two genes as a vaccine. The genes genes are two genes are two genes are two genes are two genes are two genes are two genes are two genes are two genes are two genes are two genes are two genes are two genes are two genes are two genes are two genes are two genes are two genes are two genes are two genes are two genes are two genes are two genes are two genes are two genes are two genes are two genes are two genes are two genes are two genes are two genes are two genes are two genes are two genes are two genes are two gene
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Best Local
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Alpha-D-glucosyltransferase; primer-independent; soluble glucan; sucrose; transgenic plant; cloning; Escherichia coll; phage lambda-Cl3; vector; plasmid pGSG501; plasmid pGSG502; gene transfer; crop improvement; storage carbohydrate; pasture;
                                                                                                         R91047 standard; Protein; 1577 AA.
R91047;
22-MAY-1996 (first entry)
Alpha-D-glucosyltransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-JAN-1994 (first entry)
Parainfluenza virus type 3 (PIV-3) HN protein.
PIV; RSV; multimeric; hybrid; pathogen; chimer
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06-JAN-1992; GB-000117.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CONN-) CONNAUGHT LAB LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA sequence encoding hexokinase - is used to transform organism production of enzyme claim 8; Page 14-16; 17pp; Japanese.
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12-MAR-1997; 057330.
15-MAR-1996; JP-059136.
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                                                                                                                                                                                                                                                                                                     7 LQMGATAIKQVKKLFKKWGW 26
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Pred. No. 1.10e+02;
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Pred. No. 1.10e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                         10;
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Claim 4: Page 16-20; 3lpp: English.

The sequence represents an alpha-D-glucosyltransferase from streptococcus salivarius. The enzyme is primer-independent, and produces soluble glucan from sucrose. A gene encoding the enzyme cof produces soluble glucan from sucrose. A gene encoding the enzyme may be cloned and expressed in Escherichia coli using a subclone of phage lambda-Cl3, e.g. plasmid pGSG501 or plasmid pGSG502. The DNA may also be expressed in a transgenic plant, to improve the level of stored carbohydrate in a pasture plant which normally contains low levels, or to prevent degradation of stored carbohydrate during plant senescence. Dextran may be isolated from the plant, for use as a food binder or pharmaceutical additive. Primer independence ensures that the enzyme will be functional in plants. The glucan is poorly degraded in plants but easily degraded by bacteria in the rumen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
Matches
                                                                                                                                                                                                                                     06-MAR-1997.
23-AUG-1996; IB0996.
23-AUG-1995; US-002687.
(UYBR-) UNIV BRITISH COLUMBIA.
(UYBR-) Gough M, Hancock REV
WPI; 97-179179/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24-AUG-1995; AU0527.
24-AUG-1994; AU-007643.
(GITEY) GIFFARD P M.
(JACOV) JACQUES N A.
(SIMP) SIMPSON C L.
GIffard PM. Jacques NA,
WPI: 96-151376/15.
and as a food preservative Claim 3; Page 66; 89pp; English.
                                                                                                                                                                                                                                                                                                                                                                    Antimicrobial cationic peptide CP-23.

Bacterial; viral; antitumour; food; preservative; inhibitor; growth; bacterium; yeast; endotoxaemia; sepsis; antibiotic; fungal; antiviral; Candida albicans; sterilant; Salmonella; Yersina;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of grazing
                                                                                                                                                                                                          Cationic peptide(s) having anti-microbial activity - used for the inhibition of bacterial and viral growth, as an antitumour agent,
                                                                                                                                                                                                                                                                                                                                                             Shigella
                                                                                                                                                                                                                                                                                                                                                                                                                                                 W12897 standard; peptide; 13 AA. W12897;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                      10-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plants contg. new bacterial DNA encoding glucosyl transferase activity - retain higher levels of stored carbohydrate(s) in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            feedstuff; senescence; dextran; binder; food; pharmaceutical.
Streptococcus salivarius strain ATCC 25975.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      959 iagnaklfkewg 970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31.2%;
Local Similarity 66.7%;
es 8; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14 IKQVKKLFKKWG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1577 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        livestock.
                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25
                                                                                                                                                                                                                                                        Hancock REW;
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               No ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 16;
1.10e+02;
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                                                  RESULT
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                                                                                                                                                                     Query Match 30.2%;
Best Local Similarity 47.4%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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Best Local
W61021 standa
W61021;
W61021;
13-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antibiotic resistant bacteria, combined with activity against the medically important fungus Candida albicans. In addition, the peptides are useful as antitumour agents and/or antiviral agents. The peptides may be used as sterilants or preservatives of materials susceptible to microbial or viral contamination, e.g. in processed foods to inhibit salmonella, Yersina and Shigella. The peptides are compact and tend to have a unique polyproline type II extended helix structure that permits them to span the membrane with relatively few amino acids. The peptides possess the ability to work synergistically with antibiotics, and in addition, some of then possess anti-endotoxin activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteriocin derivative
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R95262 standard; Protein; 74 AA.
                                                                                                                                                                                                                                         test substrate for Sequence 74 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Havarstein LS, Ne
WPI; 96-268604/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-MAY-1996.
16-NOV-1995; NO0213.
17-NOV-1994; NO-004411.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cleavage_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protease; restriction protease; cleavage; proteolytic domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R95262;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9616167-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HAVA/) HAVARSTEIN L S.
(NESI/) NES I F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lactococcus lactis.
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                                                                                                                                    26 qmgrdlyddddkdpkkwgw 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20 LFKKWGW 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ffkkwpw 7
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                                  standard; Protein; 128
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 (first entry)
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derivative (lactococcin G beta) peptide C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34..74
/label= Mature peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= Enterokinase cleavage site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'label- N-terminal affinity tag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ocation/Qualifiers
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                                                                                                                                                                     Score 60; D
Pred. No. 1.
1; Mismatc
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Pred. No. 1.67e+02;
1; Mismatches 1
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Streptococcus pneumoniae encoded polypeptide

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Search completed: Wed Sep 15 10:38:07 1999 Job time: 17 secs.
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                                                                                                      go.
                                                                                                                                   Query Match
Best Local S
Matches
                                                                                                                                                                                                      Procession to streptococcus pneumoniae - useful, Procession in the control of meningitis

Claim 11; Page 114; 130pp; English.

CC The sequence is that of the polypeptide encoded by a region isolated from S. pneumoniae. The protein, or agonists of it.

CC may be useful as an antibacterial for treatment or control of infection, specifically caused by S. pneumoniae or prevention of infection, specifically caused by S. pneumoniae or control of infection, or agonists of it.

CC prevention of infection, specifically caused by S. pneumoniae or control of an in-dwelling device or any other invasive procedure. The protein, or nucleic acid encoding of it. can also be used in vaccines to induce a cellular and/or humoral immune response, or to screen for other antibacterials. The DNA may also contain flanking sequences that are potential sources of control elements for bacterial can be used diagnostically, e.g. to detect a mutation for sequence 128 AA;

SQ Sequence 128 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-MAY-1998.
27-OCT-1997; U19226.
01-NOV-1996; US-029930.
(SMIK ) SMITHKLINE BEECHAM CORP.
(SMIK ) SMITHKLINE BEECHAM PLC.
Black MT, Hodgson JE, Knowles DJC, Lonetto MA, Nicholas RO, Reid RH, Zarfos PN;
WPI; 98-286586/25.
N-PSDB; V37409.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptococcus pneumoniae. WO9819689-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          infection;
                                                                                          60 ikaerdlfktw-w 71
|| : ||| | |
                                                                      14 IKOVKKLFKKWGW 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        region: ORF; open reading frame; antibacterial;
ion; prevention; meningitis.
                                                                                                                                       h 30.2%;
Similarity 53.8%;
7; Conservative
                                                                                                                                       Score 60; DB 33; Le
Pred. No. 1.67e+02;
1; Mismatches 4;
                                                                                                                                                                        Length 128;
                                                                                                                                         Indels
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在各种企业,是是一种工作,是是一种工作,是一种工作,是一种工作,是一种工作,是一种工作,是有一种工作,并有有一种工作的,是有一种工作的,是一种工作的,是一种工作的。		*************************************
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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Wed Sep 15 10:40:03 1999; MasPar time 1.59 Seconds 165.973 Million cell updates/sec Run on:

Tabular output not generated.

>US-09-068-507A-1 (1-26) from US09068507A.pep 199 Title: Description: Perfect Score: Sequence:

1 KSSAYSLQMGATAIKQVKKLFKKWGW 26

PAM 150 Gap 15 Scoring table:

106580 seqs, 10152877 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

a-issued 1:5A\_COMB 2:5B\_COMB 3:PCT9\_COMB 4:backfiles1

Mean 21.296; Variance 76.695; scale 0.278 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

		æ			SUMMAKIES		
Result No.	Score	Query	Query Match Length DB	DB	QI	Description	Pred. No.
1	71		572	-	US-08-160-	Sequence 3. Application	8.350+00
7	71	35.7	1620	7	US-08-542-	~	8.35e+00
က	9	30.5	572	7	US-08-185-	81,	8.17e+01
4	9	30.5	572	~	US-08-191-	81,	8.17e+01
S	59	6	231	~	US-08-808-	33,	9.99e+01
ø	59	29.6	316	m	PCT-US95-0	2.	9.996+01
7	59	29.6	316	7	US-08-464-	7	9.99e+01
80	59	29.6	372	4	5514582-2	$\sim$	9.99e+01
σ	59	29.6	372	~	US-08-513-	ď	9.99e+01
10	59	29.6	385	7	US-08-340-	~	9.99e+01
11	59	29.6	385	7	US-08-461-	7	9.99e+01
12	28	29.1	410	Н	US-08-073-	16,	1.22e+02
13	57	28.6	49	7	US-08-456-	26,	1.49e+02
14	57	28.6	49	~	US-08-237-	26,	1.49e+02
12	57	28.6	450	m	PCT-US95-0	7, A	1.49e+02
16	57	28.6	485	Н	US-07-991-	42,	1.49e+02
17	57	28.6	544	Н	US-08-264-	7, 4	1.49e+02
18	57	28.6	1167	Н	US-08-485-	ģ	1.49e+02
57	57	8	1167	7	us-08-290-	ý	1.49e+02
50	57	28.6	1168	7	US-08-620-	6	1.49e+02
21	57	•	1220	Н	US-08-158-	43,	1.49e+02
22	57	28.6	1220	~	US-08-611-	43,	1.49e+02
23	57	28.6	1289	4	5281530-3	5281530	1.49e+02

35.7%; Score 71; DB 1; Length 572;

Query Match

	OHTHOUSE , ,	
11.499e+002 12.499e+002 13.499e+002 14.499e+002 15.499e+002 16.499e+002 17.499e+002	S) LYMPHOMA,	
5426049. Application	DARD; PRT; 572 AA.  IS/08160861 US/08160861 US/08160861 US/08160861 US/08160861 US/08160861 US/08160861 US/08160861 US/08160861 US/08160861 US/08160,861 US/08/160,861 US/08/160	
Patent No. 5 Sequence 4, Sequence 4, Sequence 4, Sequence 4, Sequence 4, Sequence 2, Sequence 3, Sequence 3, Seque	NRT; 572 AA.  11  12  ON NUCLEIC ACID OTEINS PRESENT I  ON AND USES THE GOLDSTEIN & FOX  7 SUITE 600  10, Version #1  10, 861  10, 861	,; Z
5426049-4 US-08-158- US-08-08-158- US-08-08-316- US-08-316-	S-08-160-861-3 STANDARD; PRT; 572 AAXXXX  equence 3, Application US/08160861  Patent No. 552295  GENERAL INFORMATION: APPLICANT: MORRIS. STEPHAN W TITLE OF INVENTION: OF DETECTION NUCLEIC ATTILE OF INVENTION: OF DETECTION AND USES NUMBER OF SEQUENCES: 10  CORRESPONDENCE ADDRESS: ADDRESSEE: STERNE, RESSLER, GOLDSTEIN & STREET: 1100 NEW YORK AVE NW SUITE 600 CITY: WASHINGTON STAFE: 10.C. ZIP: AD005  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATORIN DATA: COMPUTER: O2-DEC-1993  CLASSIFICATION NUMBER: 05-065.0400000  TELECOMMUNICATION INFORMATION: NAME: MILLMAN, ROBERT A REFERENCE/DOCKET NUMBER: 0556.0400000  TELECOMMUNICATION INFORMATION: REFERENCE/DOCKET NUMBER: 12678  INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:	ids ; 1722781 CN
4	STANDARD  STANDARD  ion US/0  Kion US/0  N: STANDARD  N: STANDARD  N: STANDARD  N: STANDARD  N: STANDARD  N: STANDARD  STANDARD  E FORM: FC COMP  F	umino acid acid hear protein 52849 MW;
11133333333333333333333333333333333333	Licatic Licati	72 ami 10 aci 11nea 3: pr 7; 628
11.11.00.00.00.00.00.00.00.00.00.00.00.0	1.08-160-861-3 STANDARD;  CXXX  GGUENCE 3, Application US/081608  GQUENCE 3, Application US/081608  GENERAL INFORMATION: APPLICAMT: MORRIS: STEPHAN W TITLE OF INVENTION: OF USION PI TITLE OF INVENTION: OF DETECT NUMBER OF SEQUENCES: 10 CORRESPONDENCE ADDRESS: ADDRESSEE: STERNE, KESSLER, STREET: 1100 NEW YORK AVE; CITY: WASHINGTON STRAFE: D.C. ZIP: O1005 COMPUTER: EADABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE COMPUTER: IBM PC COMPATIBLE COMPUTER: IBM PC COMPATIBLE SOFTWARE: PATCHIN RCLEASE CURRENT APPLICATION NUMBER: US/08/: FILING DATE: 0-DEC-1993 CLASSIFICATION NUMBER: 05/08/: FILING DATE: 0-DEC-1993 TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION NUMBER: 06/08/: TELECOMMUNICATION NUMBER: 03/11-2678 INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:	LENGTH: 572 TYPE: amino TOPOLOGY: 1 MOLECULE TYPE: ENCE 572 AA;
6 6 6 6 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	Sequence 3, Applements of the control of the contro	LENGT TYPE: TOPOL MOLECUL SEQUENCE
42444444444444444444444444444444444444	XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX	
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RESULT

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Sequence 81, Application US/08191866D
Patent No. 5783195
GENERAL INFORMATION:
APPLICANT: Cochran, Mark D
APPLICANT: Macdonald, Richard D.
TITLE OF INVENTION: Recombinant Infectious Bovine
TITLE OF INVENTION: Recombinant Infectious Bovine
TITLE OF INVENTION: Recombinant Infectious Bovine
TITLE OF INVENTION: Recombinant Infectious Bovine
TITLE OF INVENTION: Recombinant Infectious Bovine
TITLE OF INVENTION: Recombinant Infectious Bovine
TITLE OF INVENTION: Recombinant Infectious Bovine
ADDRESSEE: 99
CORRESSEE: John P. White
STREET: 1185 Avenue of the Americas
CITT: New York
STATE: New York
STATE: New York
COUNTRY: USA
                                                  Sequence 81, Application US/08185949B
Patent No. 5874279
GENERAL INFORMATION:
APPLICANT: Mark D. Cochran
APPLICANT: Mark D. Cochran
APPLICANT: Richard D. Macdonald
TITLE OF INVENTION: Rhinotracheitis Virus
NUMBER OF SEGUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White
STRRET: 1185 Avenue of the Americas
CITY: New York
COUNTRY: USA
ZIP: 1005
COUNTRY: 18M YORK
COMPUTER: Ploppy disk
COMPUTER: 18M 330 466 DX2
CORPUTER: 18M 330 466 DX2
COMPUTER: 18M 304 466 DX2
CORPUTER: 103-NOV-1994
FILING DATE: 03-NOV-1994
CLASSIFICATION NUMBER: 678
REGISTRATION NUMBER: 678
TELEPHONE: (212) 278-040
TELEPHONE: (212) 278-040
TELEPHONE: (212) 278-040
TELEPHONE: CAPPERISTICS:
TENERAL OF SEQUENCE CHARACTERISTICS:
TENERAL OF SEQUENCE CHARACTERISTICS:
TENERAL OF SEQUENCE CHARACTERISTICS:
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MOLECULE TYPE: protein
JENCE 572 AA; 64607 MW; 1762281 CN;
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Sequence 81, Application US/08185949B
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                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Morris, Stephan W.
APPLICANT: LOOK, A. Thomas
TITLE OF INVENTION: ALK Protein Tyrosine Kinase/Receptor and
TITLE OF INVENTION: Ligands Thereof
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: Mashington
CITY: Washington
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/542,363
FILING DATE: 12-OCT-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: FOX, Samuel L.
REGISTRATION NUMBER: 30,353
REFERENCE/POCKET NUMBER: 0656.0400001/SLF/GKT
TELECOMMUNICATION:
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Best Local Similarity 52.4%; Pred. No. 8.35e+00;
Matches 11; Conservative 1; Mismatches 9; Indels
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Pred. No. 8.35e+00;
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MOLECULE TYPE: protein
SEQUENCE 1620 AA; 176416 MW; 13627521 CN;
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Patent No. 5770421
GENERAL INFORMATION:
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Local Similarity 52.4%;
hes 11; Conservative
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COUNTRY: US
ZIP: 20005
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Patent No. 5871992
GENERAL INFORMATION:
APPLICANT: Telebor, George W.
APPLICANT: Hilbert, Timothy P.
TITLE OF INVENTION: MANMALIAN ENDONUCLEASE III AND
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC USES THEREOF NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PatentIn PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURSENT APPLICATION DATA:
APPLICATION NUMBER: US/08/191,866D
FILING DATE: 4 February 1994
CLLASSIFICATION: 44
CLLASSIFICATION: 45
ATORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
TELEFHONE: (212) 278-0400
TELEFAN: (212) 391-0525
TELEFAN: (212) 391-0525
INFORMATION FOR SEQ ID NO: 81:
SEQUENCE CHARACTERISTICS:
LENGTH: 572 amino acid
TYPE: amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                      Query Match 30.2%; Score 60; DB 2; Length 572; Best Local Similarity 30.0%; Pred. No. 8.17e+01; Matches 6; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/808,550
FILING DATE: 26-FEB-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                       231 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1049-1-001 N
TELECOMUNICATION INFORMATION:
TELECHONE: 201-487-5800
                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE 572 AA; 64607 MW; 1762281 CN;
                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 33, Application US/08808550
                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                      432 LQLGVIDISDYNNIRINWTW 451
                                                                                                                                                                                                                                                                                                                                            7 LOMGATAIKQVKKLFKKWGW 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hackensack
: New Jersey
RY: USA
                                                                                                                                                                                                                                                                                                 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                       US-08-808-550-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE:
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GENERAL INFORMATION:
APPLICANT: HG, ET AL.
TITLE OF INVENTION: Human Prostatic Specific Reductase
NUMBER OF SEQUENCES: 8
CORRESPONDER CAPBRESS:
ADDRESSE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESSE: CECCHI, STEWART 6 OLSTEIN
STREET: 6 BECKER FARM ROAD
                                                                                                                                                                                                                                                         Score 59; DB 2; Length 231;
Pred. No. 9.99e+01;
3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: MS-DOS
SOTTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/01827A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         325800-228
                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
JENCE 316.AA; 35444 MW; 517444 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application PC/TUS9501827A
                                                                                                                                                                                                         NISM: S. cerevisiae
231 AA; 25982 MW; 264148 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: FERRARO, GREGOR D.
REGISTRATION NUMBER: 36,134
REFERRORE/DOCKET NUMBER: 3258
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 316 AMINO ACIDS
TYPE: AMINO ACID
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Concurrently
                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                       LENGIH: 231 amino acids TYPE: amino acid
                                                                                                                                                                       N-terminal
                                                                                                                                 MOLECULE TYPE: protein
HYPOTHETICAL: NO
FRAGMENT TYPE: N-termin
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 45.5%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 6 BELLALICE CITY: ROSELAND STATE: NEW JERSEY
                                                                                             STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM:
SOFTWARE: WORD PR
                                                                                                                 linear
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                                                                                                                                                                                                                                                                                                                                            161 HVHRLCKMWNW 171
                                                                                                                                                                                                                                                                                                                                                                                16 QVKKLFKKWGW 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07068
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                                                                                                                   TOPOLOGY:
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1; Gaps
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Ratent No. 5786204
GENERAL INFORMATION:
APPLICANT: HE, ET AL.
TITLE OF INVENTION: Human Prostatic Specific Reductase
NUMBER OF SEQUENCES:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
STRESSEE: CECCHI, STEWART & OLSTEIN
STREST: 6 BECCHI, STEWART
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
  Score 59; DB 3; Length 316;
Pred. No. 9.99e+01;
8; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29.6%; Score 59; DB 2; Length 316; 28.0%; Pred. No. 9.99e+01; vative 8; Mismatches 9; Indels
                                                                                                                             316 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-228
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,400
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
ETTEN APPLICATION DATA:
ETTEN APPLICATION DATA:
ETTEN AND NUMBER:
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                                                                                                                             PRT;
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MOLECULE TYPE: PROTEIN
SEQUENCE 316 AA; 35444 MW; 517444 CN;
                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
                                                226 TIYSVHPGTVQSELVRHSSFMRWMW 250
                                                                                                                                                                                              Sequence 2, Application US/08464400
                                                                       3 SAYSLOMGATAIKOVKKL-FKKWGW 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             226 TTYSVHPGTVQSELVRHSSFMRWMW 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 SAYSLQMGATAIKQVKKL-FKKWGW 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 316 AMINO ACIDS TYPE: AMINO ACID
                                                                                                                         STANDARD;
Query Match
Best Local Similarity 28.0%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 28.0%;
7; Conservative
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                                                                                                                     US-08-464-400-2
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TD 5514582-2
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Gaps
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                                                              APPLICANT CAPON, DANIEL J.;LASKY, LAURENCE A.
TITLE OF INVENTION: RECOMBINANT DNA ENCODING HYBRID
IMMUNGLOBULINS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/185,670
FILING DATE: 21-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 986,931
FILING DATE: 16-DEC-1992
APPLICATION NUMBER: 808,122
FILING DATE: 16-DEC-1991
C FILING DATE: 12-NOV-1989
C APPLICATION NUMBER: 810,122
FILING DATE: 22-NOV-1989
C APPLICATION NUMBER: 315,015
C APPLICATION NUMBER: 315,015
C APPLICATION NUMBER: 315,015
                                                                                                                                                                                                                                                                                                     Score 59; DB 4; Length 372;
Pred. No. 9.99e+01;
                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: LASKY, LAURENCE A.
APPLICANT: STACHELL, SCOTT E.
APPLICANT: STACHELL, SCOTT E.
APPLICANT: STACHELL, SCOTT E.
APPLICANT: STROER, MEK S.
TITLE OF INVENTION: LYMPHOCYTE HOMING RECEPTORS
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genenteeh, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                           2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: parin (Generación Correster)
CURRENT APPLICATION DATA:
PILING DATE: US-08/513,278
FILING DATE: 10-AUG-1995
CLASSIFICATION: 5310
PRIOR APPLICATION: DATA:
APPLICATION NUMBER: 08/059027
                                                                                                                                                                                                                                                                           403 AA; 45623 MW; 933915 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/08513278
Patent No. 5840844
GENERAL INFORMATION:
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06-MAY-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/08513278
                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                     Ouery Match
Best Local Similarity 62.5%;
                                                                                                                                                                                                                                                                                                                            5; Conservative
                                 Patent No. 5514582.
                                                        Patent No. 5514582
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                                                                                                                                                                                                                                                   SEQ ID NO:2:
LENGTH: 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
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19 KLFKKWGW 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-513-278-2
           01-JAN-1900
                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                   Ouery Match
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Matches
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Patent No. 5808025
GENERAL INFORMATION:
APPLICANT: Tedder, Thomas F.
APPLICANT: Ransas, Geoffrey.
TITLE OF INVENTION: GHIMPRIC SELECTINS AS SIMULTANEOUS
TITLE OF INVENTION: BLOCKING AGENTS FOR COMPONENT SELECTIN FUNCTION
TITLE OF INVENTION: BLOCKING AGENTS FOR COMPONENT SELECTIN FUNCTION
NUMBER OF SEQUENCES: 28
CORRESPONDED ADDRESS:
APPROPRIED OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF T
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21P: 10020
COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.30
SOPTWARE: PatentIn Release #1.0, Version #1.30
SOFTWARE: 16-NOV-1994
TLING DATE: 16-NOV-1994
TLING DATE: 16-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                     Query Match 29.6%; Score 59; DB 2; Length 372; Best Local Similarity 62.5%; Pred. No. 9.99e+01; Atches 5; Conservative 2; Mismatches 1; Indels Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 385 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TAME: Gunnison, Jane
REGISTRATION NUMBER: 38,479
REFERENCE/DOCKET NUMBER: CG-104 CON
REFERENCE/DOCKET NUMBER: CG-104
TELEPHONE: 212-596-9000
TELEPAX: 212-596-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: FISH & NEAVE STREET: 1251 Avenue of the Americas CIIY: New York STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/008,459
FILING DATE: 25-JAN-1993
ATTORNEX/AGENT INFORMATION:
                                                                                                                      ATTOWNED FORTER

ATTOWNED FORTER

REGISTRATION NUMBER: 365DLCI
RELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPAN: 415/952-981
TELEFAX: 910/371-7168
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 372 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                      372 AA; 42209 MW; 729258 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/08340539A
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                   FILING DATE: 31-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/315015
07/786149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                          FILING DATE: 23-FEB-1989
ATTORNEY/AGENT INFORMATION:
      APPLICATION NUMBER: 07/78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-340-539A-2
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Sequence 2, Application US/08461592B
Patent No. 5834425
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Tedder, Thomas F.
APPLICANT: Ransas, Geoffrey S.
APPLICANT: TRANSAS, GEOFFREY S.
APPLICANT: TRANSAS, GEOFFREY S.
APPLICANT: SELECTIN FUNCTION
TITLE OF INVENTION: BLOCKING AGENTS FOR COMPONENT SELECTIN FUNCTION
TITLE OF INVENTION: BLOCKING AGENTS FOR COMPONENT SELECTIN FUNCTION
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Weingarten, Schurgin, Gagnebin & Hayes
STREET: Ten Post Office Square
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                                                                                                                                                                                        Gaps
                                                                                                                                                                                          ö
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Pred. No. 9.99e+01;
                                                                                                                                          Score 59; DB 2; Length 385; Pred. No. 9.99e+01; 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOGTWARE: Patentin Release #1.0, Version #1.25
SOGTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,592B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PILING DATE: 25-JAN-1993
ATTORNEY AGENT INFORMATION:
NAME: James F. Haley, Jr.
REFERENCE/COKET NUMBER: 27,794
REFERENCE/COKET NUMBER: CG-104
REFERENCE/COKET NUMBER: CG-104
TELEPHONE: (212) 596-9000
TELEPHONE: (212) 596-9000
TELEPHONE: (212) 596-9000
TELEPHONE: (212) 596-9000
TELEPHONE: (212) 596-9000
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TELEPHONE: (312) 596-9000
TELEPHONE: (312) 596-9000
TELEPHONE: (312) 596-9000
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/340,539
FILING DATE: 16-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/008,459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
JENCE 385 AA; 43743 MW; 775024 CN;
                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
OFFERTING SYSTEM:
                                                            TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE 385 AA; 43743 MW; 775024 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/08461592B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 62.5%;
                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                 385 amino acids
amino acid
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                         y Match 29.6%;
Local Similarity 62.5%;
les 5; Conservative
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SEQUENCE
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          Gaps
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                                                                                                          Sequence 16, Application US/08073807A
Patent No. 5646248
GENERAL INFORMATION:
APPLICANT: Sawada, Ritsuko
APPLICANT: Lowe, John B.
TILLE OF INVENTION: GELL SURFACE LAMP EXPRESSION
TITLE OF INVENTION: SELECTIN-DEPENDENT ADHESION
CORRESPONDENCE 3.18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 470 La Jolla Village Drive, Suite 700
   2; Mismatches 1; Indels
                                                                                                                                                                                                                        COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/073,807A
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                       'Match 29.1%; Score 58; DB 1; Length 410; Local Similarity 28.6%; Pred. No. 1.22e+02; 6; Conservative 5; Mismatches 10; Indels
                                                              410 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49 AA.
                                                                                                                                                                                                                                                                                            NAME: Cambell, Caltryn A. REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 9567
TELECOMUNICATION INFORMATION:
TELEPHONE: (619) 535-8949
INFORMATION FOR SEQ ID NO: 16:
                                                             PRT;
                                                                                              Sequence 16, Application US/08073807A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
NCE 410 AA; 44988 MW; 908539 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 26, Application US/08456647B
                                                          STANDARD;
                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                       California
: United States
                                                                                                                                                                                                                                                                                                                                                        1: 410 amino acids amino acids
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5; Conservative
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US-08-073-807A-16
            29 NIFKLWGW 36
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19 KLFKKWGW 26
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US-08-456-647B-26
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,647B
CLASSIFICATION 530
APPLICATION S30
APPLICATION NUMBER: US/08/237,401
FILING DATE: 02-May-1994
APPLICATION NUMBER: US/08/237,401
FILING DATE: 12-May-1997
APPLICATION NUMBER: US/08/237,401
APPLICATION NUMBER: US/08/237,401
APPLICATION NUMBER: US/08/237,401
APPLICATION NUMBER: US/08/237,401
APPLICATION NUMBER: US/08/237,401
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APPLICATION NUMBER: US/08/237,401
APPLICATION NUMBER: US/08/237,401
APPLICATION NUMBER: US/08/237,401
APPLICATION NUMBER: US/08/237,401
Sequence 26, Application US/08456647B
Patent No. 5811516
GENERAL INFORMATION:
APPLICANT LEMBE Ph.D. et al., Greg E.
ITILE OF INVENTION:
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson p.C.
STREET: 4225 Executive Square, Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28.6%; Score 57; DB 2; Length 49; 33.3%; Pred. No. 1.49e+02; vative 6; Mismatches 10; Indels
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Patent No. 5837448
GENERAL INFORMATION:
APPLICANT: Lemke Ph.D. et al., Greg E.
TITLE OF INVENTION: PROTEIN-TYROSINE KINASE GENES
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
CITY: La Jolla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07251/007002
                                                                                                                                                                                                                                                                                                                           MEDIUM TIPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Wetherell Ph.D. John R. REGISTRATION UNABER: 31,678
REFERENCE/DOCKET NUMBER: 07251/06
TELECOMMUNICATION INFORMATION: (619) 678-5070
INFORMATION FOR SEQ ID NO: 26;
SEQUENCE CHARACTERISTICS: 75NCTH CARRACTERISTICS: 75NCTH CARRACTERISTICS: 75NCTH CARRACTERISTICS: 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LE TYPE: protein
49 AA; 5339 MW; 14108 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 26, Application US/08237401A
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                                                                                                                                                                                                                                                                             ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49 amino acids
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les 8; Conservative
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OGY: linear
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                                                                                                                                                                                                                                                            COUNTRY:
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STATE: C!
COUNTRY:
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Search completed: Wed Sep 15 10:40:11 1999
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APPLICANT: Sugen, Inc.
APPLICANT: 515 Galveston Drive
APPLICANT: 15 Galveston Drive
APPLICANT: Redwood City, California 94063-4720
APPLICANT: Redwood City, California 94063-4720
APPLICANT: Wisenschaften E.V.
APPLICANT: Hofgarten Str. 2
APPLICANT: Munchen 80539
APPLICANT: Germany
TITLE OF INVENTION: Novel Megakaryocytic Protein Tyrosine
TITLE OF INVENTION: Kinases
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS: 21
CORRESPONDENCE ADDRESS: 21
                                                                                                                                                                                                                                                                                                                                                     Query Match 28.6%; Score 57; DB 2; Length 49;
Best Local Similarity 33.3%; Pred. No. 1.49e+02;
Matches 8; Conservative 6; Mismatches 10; Indels
                 COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC Compatible
COMPUTER: TBM PC COMPATION
COMPUTER: TBM PC POSYMS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/237,401A
RPLICATION NUMBER: US/08/237,401A
APPLICATION NUMBER: US/08/237,401A
APPLICATION NUMBER: US/08/237,401A
RPLING DATE: 15-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Halle Ph.D. Lise A.
REGISTRATION NUMBER: 38,347
REGISTRATION NUMBER: 38,347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible COMPUTER: OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    450 AA.
                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 07251/007001
TELEPHONE: (619) 678-5070
TELEPHONE: (619) 678-5070
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 49 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IISS Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 7, Application PC/TUS9505008
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 7, Application PC/TUS9505008
                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
JENCE 49 AA; 5339 MW; 14108 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                            11 KVSDFGLTKEASSTQDTGKLPVKW 34
                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: New York COUNTRY: U.S.A. ZIP: 10036
                                                                                                                                                                                                                                                                                                TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
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PCT-US95-05008-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: unknown
MOLECULE TYPE: protein
JENCE 450 AA; 50704 MW; 1071733 CN;
                                                                                                                                                                  APPLICATION NUMBER: US 08/232,545
FILING DATE: 22-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7683-074
                                                                                                                                                                                                                                                                                             CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, LGURA A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7683-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)790-9991
TELEFA: (212)869-9741
TELEFA: (212)869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 450 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: AUGUSTRATION ACIDS
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                                                   CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               unknown
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protein - protein database search, using Smith-Waterman algorithm Wed Sep 15 10:38:24 1999; MasPar time 4.14 Seconds 251.685 Million cell updates/sec

Tabular output not generated.

>US-09-068-507A-1 (1-26) from US09068507A.pep 199 1 KSSAXSLOMGATAIKOVKKLFKKWGW 26 Title:

Description: Perfect Score: Sequence:

PAM 150 Gap 15 Scoring table:

Searched:

122810 segs, 40068593 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

pir60 1:pirl 2:pir2 3:pir3 4:pir4 Database:

Mean 31.155; Variance 49.460; scale 0.630 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Pred. No.	5.88e-20	7.06e-02	1.56e-01	2.30e-01	2.30e-01	٠	2.25e+00	3.25e+00	3.25e+00	3.25e+00	4.68e+00	4.68e+00	6.70e+00	6.70e+00	6.70e+00	9.58e+00	1.36e + 01	1.36e+01	1.93e+01	1 936+01	1000	-	÷,	1.936+01
Description	plantaricin A - Lacto	probable membrane pro	L-iduronidase (EC 3.2	hypothetical protein	qamma-aminobutyric ac	virc-region hypotheti	bo-type ubiquinol oxi	dedA protein - Mycoba	hypothetical protein	gene 38 protein - pha	hypothetical protein	hypothetical protein	conserved hypothetica	cerebrin-50 - human	NAD+ ADP-ribosyltrans	creatine kinase (EC 2	transcription regulat	hypothetical protein	conserved hypothetica	Opening the property of the pr	reverse cramscraped	eno) nomor	gene T48 protein - ir	lanosterol 14alpha-de
ID	A45913	S25345	A42420	D71021	JE0356	A40361	B38129	572727	C71060	541185	531236	A71174	F69771	T52374	542208	A27708	T39841	571638	10000	11000	PH0ZI/	C69391	542989	JC4240
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* Query Match Length	22	1609	655	0.50	960	32	649	134	157	2010	341	457	246	7 7	900	400	200	1 0	יו פר	707	340	366	419	486
% Query Match	83.4	30.0	38.5	2.7.5	37.7	. 5.	3.4.7	2.45			2				4.0	30.6				31./	31.7	31.7	31.7	31.7
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521976 521347 516783 516783 516783 5216783 5216460 702295 701163 522481 8225481 8225481 8225481 810163 8101
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### ALIGNMENTS

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um -1993 #te:	Sletten,	abase, Ap	#checksum 9237	ength 22; Indels
ıs plantar olantarum lon 14-May	rsen, A.;	quence Dat		Score 166; DB 2; Length 22; Pred. No. 5.88e-20; 0; Mismatches 0; Indels
<pre>#type complete A - Lactobacillu e Lactobacillus   #sequence_revis: 97</pre>	Granly-La:	rotein Se	NIS :locin :ular-weig	ore 166; ed. No. 5 ); Mismat
A45913 #type complete plantaricin A - Lactobacillus plantarum #formal_name Lactobacillus plantarum 14-may-1993 #text_change 12-Sep-1997	A45913 A45913 Nissen-Meyer, J.; Granly-Larsen, A.; Sletten, K.; Daeschel, M.: Nes. I.F.	submitted to the Protein Sequence Database, April 1993 A45913 preliminary	type protein 1-22 ##label NIS antibiotic; bacteriocin #length 22 #molecular-weight 2497	
A45913 #ty plantaricin A #formal_name 1 14-May-1993 #ty 12-Sep-1997	A45913 A45913 Nissen-h	submitte A45913 pre	_type pr 1- antibio #length	83.4%, Similarity 100.0%, 22; Conservative
RESULT 1 ENTRY TITLE ORGANISM DATE	ACCESSIONS REFERENCE #authors	#submission #accession ##status	##molecule_type protein ##residues 1-22 ##1 KEYWORDS antibiotic; k SUMMARY #length 22 #	Query Match 83.4%; Best Local Similarity 100.0%; Matches 22; Conservative

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\$25345 #type complete probable membrane protein YCR089w - yeast (Saccharomyces cerevisiae)	hypothetical protein YCR1102 #formal_name Saccharomyces cerevisiae 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 06-Feb-1998	S55345; S19504 S25345; C.; Grisanti, P.; Frontali, L.	yeast (1992) 8:569-575 The complete sequence of a 6146 bp fragment of Saccharomyces The complete sequence of a 6146 bp fragment of saccharomyces cerevisiae chromosome III contains two new open reading	frames. #cross-references WUID:92397594 #accession S25345 ##molocula type DNA	###residues 1-1609 ##label WIL ##residues
RESULT 2 ENTRY TITLE	ALTERNATE_NAMES ORGANISM DATE	ACCESSIONS REFERENCE #authors	#journal #title	frame #cross-references MUI #accession \$25345 ##mologije tyno DN	##residues ##cross-ref

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #domain transmembrane #status predicted #label TMI\
#domain transmembrane #status predicted #label TM2
#length 1609 #molecular-weight 166047 #checksum 8346
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L-iduronidase (EC 3.2.1.76) - dog
#formal_name Canis lupus familiaris #common_name dog
17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change
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                                                                 Frontali, L.; Grisanti, P. submitted to the Protein Sequence Database, March 1992
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hyporhetical protein PH1465 - Pyrococcus horikoshii
#formal_name Pyrococcus horikoshii
14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change
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#title Cloning and characterization of cDNA encoding canine alpha-L-iduronidase. mRNA deficiency in mucopolysaccharidosis I dog.
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glycosidase; hydrolase; polysaccharide degradation
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Pred. No. 7.06e-02;
8; Mismatches 7; Indels
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8; Mismatches 8; Indels
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##cross-references GB:M81893; NID:g163964
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#map_position 3R
KEYWORDS
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PID:91907227
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##cross-references GB:AP000006; NID:93236133; PID:d1031515; PID:93257889
##experimental_source strain OT3
##note this accession replaces an interim accession for a
sequence replaced by GenBank
Hino, Y.; Yamamoto, S.; Sekine, M.; Baba, S.; Kosugi, H.; Hosoyama, A.; Nagai, Y.; Sakai, M.; Ogura, K.; Otsuka, R.; Nakazawa, H.; Takamiya, M.; Ohiuu, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi, A.; Aoki, K.; Yoshizawa, T.; Nakamura, Y.; Robb, F.T.; DNA Res. (1998) 5:55-76 Complete sequence and gene organization of the genome of a hyper-thermophilic archaebacterium, Pyrococcus horikoshii
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translation not shown
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Pred. No. 2.30e-01;
3; Mismatches 2; Indels
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#accession JE0356
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Local Similarity 58.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Glaser, P.; Kunst, F.; Arnaud, M.; Coudart, M.P.; Gonzales, W.; Hullo, M.F.; Ionescu, M.; Lubochinsky, B.; Marcelino, W.; Hullo, M.F.; Ionescu, E.; Santana, M.; Schneider, E.; Schweizer, I.; Presecan, E.; Santana, M.; Schneider, E.; Schweizer, J.; Vertes, A.; Rapoport, G.; Danchin, A. Mol. Microbiol. (1993) 10:371-384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Santana, M.; Kunst, F.; Hullo, M.F.; Rapoport, G.; Danchin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #authors Michiels, T.; Vanooteghem, J.C.; Lambert de Rouvroit, C.; China, B.; Gustin, A.; Boudry, P.; Cornells, G.R. China, B.; Gustin, A.; Boudry, P.; Cornells, G.R. Hjournal J. Bacteriol. (1991) 173:4994-5009 f. f. Analysis of virc, an operon involved in the secretion of Yop proteins by Yersinia enterocolitica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ##cross_references GB:M86548; NID:9143395; PID:9143397
##cross_references GB:M86548; NID:9143395; PID:9143397
##note sequence extracted from NCBI backbone (NCBIN:103632,
NCBIP:103603)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           B38129 #type complete (EC 1.10.3.-) chain I - Bacillus bo-type ubiquinol oxidase (EC 1.10.3.-)
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                                                                                                                                                                                                                                                                                                                                                                                               A40361 #type complete vicc-region hypothetical protein yscA - Yersinia virc-region hypothetical protein prv enterocolitica plasmid prv #formal_name Yersinia enterocolitica formal_ame Yersinia enterocolitica 21-Feb-1992 #sequence_revision 21-Feb-1992 #sequence_revision 21-Feb-1992 #sequence_revision 21-Feb-1992 #sequence_revision 21-Feb-1992 #sequence_revision 21-Feb-1992 #sequence_revision 21-Feb-1992 #sequence_revision 21-Feb-1992 #sequence_revision 21-Feb-1992 #sequence_revision 21-Feb-1992 #sequence_revision 21-Feb-1992 #sequence_revision 21-Feb-1992 #sequence_revision 21-Feb-1992 #sequence_revision 21-Feb-1992 #sequence_revision 21-Feb-1992 #sequence_revision 21-Feb-1992 #sequence_revision 21-Feb-1992 #sequence_revision 21-Feb-1992 #sequence_revision 21-Feb-1992 #sequence_revision 21-Feb-1992 #sequence_revision 21-Feb-1992 #sequence_revision 21-Feb-1992 #sequence_revision 21-Feb-1992 #sequence_revision 21-Feb-1992 #sequence_revision 21-Feb-1992 #sequence_revision 21-Feb-1992 #sequence_revision 21-Feb-1992 #sequence_revision 21-Feb-1992 #sequence_revision 21-Feb-1992 #sequence_revision 21-Feb-1992 #sequence_revision 21-Feb-1992 #sequence_revision 21-Feb-1992 #sequence_revision 21-Feb-1992 #sequence_revision 21-Feb-1992 #sequence_revision 21-Feb-1992 #sequence_revision 21-Feb-1992 #sequence_revision 21-Feb-1992 #sequence_revision 21-Feb-1992 #sequence_revision 21-Feb-1992 #sequence_revision 21-Feb-1992 #sequence_revision 21-Feb-1992 #sequence_revision 21-Feb-1992 #sequence_revision 21-Feb-1992 #sequence_revision 21-Feb-1992 #sequence_revision 21-Feb-1992 #sequence_revision 21-Feb-1992 #sequence_revision 21-Feb-1992 #sequence_revision 21-Feb-1992 #sequence_revision 21-Feb-1992 #sequence_revision 21-Feb-1992 #sequence_revision 21-Feb-1992 #sequence_revision 21-Feb-1992 #sequence_revision 21-Feb-1992 #sequence_revision 21-Feb-1992 #sequence_revision 21-Feb-1992 #sequence_revision 21-Feb-1992 #sequence_revision 21-Feb-1992 #sequence_revision 21-Feb-1992 #sequence_revision 21-Feb-1992 #sequence_revision 21-Feb-199
                                                                                                                                          Gaps
#length 960 #molecular-weight 108148 #checksum 3766
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#length 32 #molecular-weight 3815 #checksum 9835
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ##residues 1-32 ##label MIC 155549; PID:g155550 ##cross-references GB:M74011; NID:g155549; PID:g155550
                                                                         / Match 37.7%; Score 75; DB 2; Length 960; Local Similarity 87.5%; Pred. No. 2.30e-01; Indels tes 7; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 70; DB 2; L4
Pred. No. 1.55e+00;
6; Mismatches 5;
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##molecule_type 1-649 ##label SAN
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Guery Match
Best Local Similarity 31.3%;
Matches 5; Conservative
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Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.W.;
Alloni, G.; Azevedo, V.; Bertero, M.G.; Besateres, P.;
Alloni, A.; Borchert, S.; Boriss, R.; Boursler, L.; Brans,
Bolotin, A.; Bergnell, S.C.; Bron, S.; Brouillet, S.;
A.; Braun, M.; Brignell, S.C.; Bron, S.; Brouillet, S.;
Bruschi, C.V.; Caldwell, B.; Capueno, V.; Carter, N.M.;
Codani, J.J.; Connerton, I.F.; Cummings, N.J.;
Chol, S.W.; Codani, J.J.; Connerton, I.F.; Cummings, N.J.;
Chol, S.W.; Demisor, F.; Devine, K.W.; Galleron, J.;
Enrich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.;
Enrich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.;
Enrich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.;
K.; Fabret, C.; Ferrari, E.; Foulger, D.; Fritz, C.; Fullta,
S.Y.; Glaser, Y.; Fuma, S.; Gallzzi, A.; Galleron, N.; Ghim,
K.; Laptud, A.; Hilbert, H.; Holsappel, S.; Hosono, S.;
C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.;
C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Koramata, D.;
Kuilta, K.; Lapidus, A.; Modlas, S.; Kumano, M.;
Kasahara, Y.; Kalerr-Blanchard, M.; Klauber, J.;
Kuilta, K.; Lapidus, A.; Lardinois, S.; Lauber, J.;
Kuilta, K.; Lapidus, A.; Mediae, N.; Liu, H.; Masuda, S.;
Kuilta, K.; Lapidus, A.; Mediae, N.; Liu, H.; Masuda, S.;
Kuilta, K.; Lapidus, A.; Odback, M.; Noone, D.; O'Really,
M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Rackott, G.;
A.W.; Prescent, E.; Pujic, P.; Purnelle, B.; Rackott, G.;
Schleich, S.; Schrocter, R.; Scoffone, F.; Sektyuchi, H.;
Fackemaru, R.; Takeudi, M.; Takeudi, A.; Takeudich, M.; Takenaru, R.; Takeudich, M.; Takenaru, R.; Takeudich, M.; Takeudich, M.; Takeudich, M.; Takeudich, M.; Takeudich, M.; Vanier, R.; Vashikawa, H.F.; Zumstein, E.;
Wangenbol, M.; Pareconi, E.; Pakagur, H.; Sammoto, W.; Varien, W.; Vashikawa, H.F.; Zumstein, R.; Vashikawa, H.F.; Zumstein, R.;
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#domain cytochrome-c oxidase chain I homology #label
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#domain transmembrane #status predicted #label TM3/
#domain transmembrane #status predicted #label TM4
#domain transmembrane #status predicted #label TM5/
#domain transmembrane #status predicted #label TM5/
#domain transmembrane #status predicted #label TM6/
#domain transmembrane #status predicted #label TM6/
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#superfamily cytochrome-c oxidase chain I; cytochrome-c
oxidase chain I homology
chromoprotein; copper binding; electron transfer; heme;
heterotetramer; membrane-associated complex;
#title Bacillus subtilis genome project: cloning and sequencing of the 97 kb region from 325 degrees to 333 degrees. #cross-references MUID:95020537
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                                                                                                                                                                ##molecule_type_DNA
##mesidues
1-649 ##label GLA
##residues
##residues EMBL:X73124; NID:9413923; PID:9413962
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Nature (1997) 390:249-256
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#domain transmembrane #status predicted #label TM8\
#domain transmembrane #status predicted #label TM9\
#domain transmembrane #status predicted #label TM10\
#domain transmembrane #status predicted #label TM10\
#domain transmembrane #status predicted #label TM11\
#binding_site heme a iron (His) (axial ligands) #status
#binding_site copper (His) #status predicted\
#binding_site heme a iron (His) (axial ligands) #status
#binding_site heme a3 iron (His) (axial ligand) #status
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Hino, Y.; Yamamoto, S.; Sekine, M.; Baba, S.; Kosuqi, H.;
Haosyama, A.; Nagai, Y.; Sakai, M.; Ogura, K.; Otsuka, R.;
Ranaka, T.; Kudoh, Y.; Samazaki, J.; Funahashi, T.;
A.; Aoki, K.; Yoshizawa, T.; Nakamura, Y.; Robb, F.T.;
Horikoshi, K.; Masuchi, Y.; Shizuya, H.; Kikuchi, H.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                $72727  #type complete
dedA protein - Mycobacterium leprae
#177_C2_172 protein
#formal_name Mycobacterium leprae
19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change
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hypothetical protein PH1177 - Pyrococcus horikoshii
#formal_name Pyrococcus horikoshii
14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change
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                                                                                                                                                                                        #length 649 #molecular-weight 73838 #checksum 999
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                                                                                                                                                                                                                                                         Score 69; DB 2; Length 649;
Pred. No. 2.25e+00;
4; Mismatches 8; Indels
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34.2%; Score 68; DB 2; Length 134;
Best Local Similarity 28.6%; Pred. No. 3.25e+00;
Matches 6; Conservative 8; Mismatches 7; Indels
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                                                                                                                                                                                                                                                         Local Similarity 42.98;
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589-605
608-624
102,417
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##moctacture_ryre run
##scosdues
1157 ##acoss-references GB:APO00005; NID:g3236132; PID:d1031220; PID:g3257594
##experimental_source strain OT3
##note this accession replaces an interim accession for a
sequence replaced by GenBank
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Analysis of cis and trans acting elements regulated for the lattiation of DNA replication in the Bacillus subtilis "Across-references Muldistated".
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#formal_name phage SPP1
20.Feb-1995 #sequence_revision 20-Feb-1995 #text_change
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Yeast (1993) 9:351-361
Molecular genetics in Saccharomyces kluyveri: the HIS3
homolog and its use as a selectable marker gene in S.
kluyveri and Saccharomyces cerevisiae.
       Preliminary; nucleic acid sequence not shown;
translation not shown
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Y # #length 256 #molecular-weight 29998 #checksum 6866
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34.2%; Score 68; DB 2; Length 157;
Best Local Similarity 30.0%; Pred. No. 3.25e+00;
Matches 6; Conservative 7; Mismatches 7; Indels
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Pred. No. 3.25e+00;
4; Mismatches 4; Indels
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33.7%; Score 67; DB 2; Length 341;
Matches 6; Conservative 5; Mismatch.
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5; Mismatches 2; Indels
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#length 341 #checksum 822
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1-256 ##label PE2
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Best Local Similarity 38.5%;
Matches 5; Conservative
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                                  ##molecule_type DNA
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Alloni, G.; Azevedo, V.; Bertero, M.G.; Bessleres, P.;
Alloni, G.; Azevedo, V.; Bertero, M.G.; Bessleres, L.; Brans, Bolotin, A.; Berchert, S.; Bronis, S.; Brouillet, S.; Brouillet, S.; Brouillet, S.; Brouillet, S.; Brouillet, N.M.; Bridwell, B.; Caphano, V.; Carter, N.M.; Caldwell, B.; Caphano, V.; Carter, N.M.; Daniel, R.A.; Denizot, F.; Devine, K.D.; Esterboeft, A.; Daniel, R.A.; Denizot, F.; Devine, K.D.; Eritz, C.; Fulta, Enrington, J.; Ennerson, P.T.; Entian, K.D.; Eritz, C.; Fulta, Enrington, J.; Ennerson, P.T.; Entian, K.D.; Fritz, C.; Fulta, S.; Fulta, C.; Kobayashi, Kasahara, Y.; Klaetr-Blanchard, M.; Klaeln, C.; Kobayashi, Kuitta, K.; Lapidus, A.; Landinois, S.; Lauber, J.; Kuitta, K.; Lapidus, A.; Lardinois, S.; Lauber, J.;
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Kawarabayasi, Y.; Sawada, M.; Horikawa, W.; Kosugi, H.;
Hino, Y.; Yamamoto, S.; Sekine, M.; Ogura, K.; Otsuka, R.;
Hosoyama, A.; Nagai, Y. Sakai, M.; Ogura, K.; Funahashi, T.;
Nakazawa, H.; Takamiya, M.; Ohfuku, Y.; Rushida, N.; Oguch,
Nakazawa, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguch,
A.; Aoki, K.; Yoshizawa, T.; Nakamira, Y.; Robb, F.T.;
Horikoshi, K.; Masuchi, Y.; Shizuya, H.; Kikuchi, H.
Horikoshi, K.; Masuchi, Y.; Shizuya, H.; Kikuchi, H.
Complete Sequence and gene organization of the genome of a
hyper-thermophilic archaebacterium, Pyrococcus horikoshii
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Matches 5; Conservative
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133 SQVKSLRKVFKKW 145
                                                                           12 TAIKOVKKLFKKW 24
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Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.;
Maueel, C.; Medigue, C.; Media, N.; Mellado, R.P.; Mizuno,
M.; Mosawa, K.; Ogiawara, A.; Noback, M.; Noone, D.; O'Rellly,
M.; Ogawa, K.; Ogiawara, A.; Oudega, B.; Perk, S.H.; Perrot,
V.; Pohl, T.M.; Portetelle, D.; Porvolik, S.; Rescott,
V.; Pohl, T.M.; Portetelle, D.; Purnelle, B.; Repoport, G.;
Rey, M.; Reynolds, S.; Reger, M.; Sado, T.; Sckalguch, E.;
Rey, M.; Reynolds, S.; Schoeler, E.; Sckalguch, J.;
Schheich, S.; Schoeler, R.; Scoffone, F.; Sckalguch, J.;
Schoeler, S.; Schoeler, R.; Scoffone, F.; Sckalguch, H.;
Schoeler, S.; Schoeler, R.; Scoffone, F.; Sckalguch, H.;
B.; Sorokin, A.; Tacconi, E.; Takada, T.;
B.; Sorokin, A.; Tacconi, E.; Takada, T.;
B.; Sorokin, A.; Tacconi, E.; Takada, T.;
B.; Sorokin, A.; Tacconi, M.; Tamakoshi, A.; Tanakoshi, H.;
Taramaru, K.; Takauchi, M.; Tosato, V.; Uchiyama, S.;
Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, S.;
Terpstra, P.; Toshida, R.; Yasarotti, A.; Yamane, K.; Yasumoto,
Wandutt, R.; Wedler, E.; Wedler, H.; Weizeneger, T.;
Vandenbol, W.; Yashikawa, H.F.; Zumstein, E.;
K.; Tata, K.; Yoshida, R.; Yoshikawa, H.F.; Zumstein, E.;
K.; Tata, K.; Yoshida, R.; Yoshikawa, H.F.; Zumstein, E.;
Mature (1997) 390:249-256
Bactilus subtilis
##cross-references MID:98044033
##cross-references MID:98044033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #authors Li, A.H.; Silvestrini, B.; Leone, M.G.; Giacomelli, S.;

#journal Carbin-50, a human cerebrospinal fluid protein whose mRNA title is present in multiple tissues but predominantly expressed in the lymphoblastoid cells and the brain.

#cross-references MUID:95253026

#accession 152374
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02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
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##molecule_type mRNA
1-435 ##residues
##residues
##cross-references GB:S76853; NID:9913522; PID:9913523
##cross-references GB:S76853; NID:9913522;
##cross-references GB:S76853; NID:9913522;
##cross-references GB:S76853; NID:9913522;
##cross-references GB:S76853; NID:9913522;
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Pred. No. 6.70e+00;
6; Mismatches 1;
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Iocal Similarity 52.9%;
hes 9; Conservative
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Wed Sep 15 10:38:57 1999; MasPar time 3.11 Seconds 236.414 Million cell updates/sec Run on:

protein - protein database search, using Smith-Waterman algorithm

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Tabular output not generated.

>US-09-068-507A-1 (1-26) from US09068507A.pep 199 Description: Perfect Score: Title:

1 KSSAYSLQMGATAIKQVKKLFKKWGW 26

PAM 150 Gap 15 Scoring table:

Sequence:

77977 seqs, 28268293 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

1:swissprot swiss-prot37 Database:

Mean 31.897; Variance 43.884; scale 0.727 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Pred. No.	5.90e-32	1.20e-02	2.93e-02	3.91e-01	5.93e-01	8.97e-01	1.35e+00	1.35e+00	2.02e+00	3.02e+00	4.48e+00	6.62e+00	9.73e+00	9.736+00	9.73e+00	9.73e+00	9.73e+00						
Description	BACTERIOCIN PLANTARICI	FACTOR INDUCED GENE 2.	ALPHA-L-IDURONIDASE PR	$^{\circ}$	QUINOL OXIDASE POLYPEP	HYPOTHETICAL 14.2 KD P	INTIMIN (OUTER MEMBRAN	HYPOTHETICAL PROTEIN I	POLY [ADP-RIBOSE] POLY	CREATINE KINASE, SARCO	HYPOTHETICAL TRANSCRIP		HYPOTHETICAL 12.0 KD P	GLUTATHIONE S-TRANSFER	HEAT SHOCK FACTOR PROT	HEMAGGLUTININ-NEURAMIN	HEMAGGLUTININ-NEURAMIN	HEMAGGLUTININ-NEURAMIN	HEMAGGLUTININ-NEURAMIN	HEMAGGLUTININ-NEURAMIN	HEMAGGLUTININ-NEURAMIN	HEMAGGLUTININ-NEURAMIN	GENE 31 PROTEIN (GP31)
А	PLNA_LACPL	FIG2_YEAST	IDUA_CANFA	YSCA_YEREN	QOX1_BACSU	YOO7_MYCLE	EAEA_HAFAL	YHS3_SACKL	PPOL_SARPE	KCRS_CHICK	YBBB_BACSU	VCAP_HSVEB	YMI4_YEAST	GTA1_RAT	HSF8_LYCPE	HEMA_PI3HW	HEMA_PI3HA	HEMA_PI3HU	HEMA_PI3H4	HEMA_PI3HV	HEMA_PI3HT	HEMA_PI3HX	VG31_BPMD2
DB	н	П	_	-	г	П	7	Н	Н	H	М	Н	Н	Н	Н	Н	Н	-	-	-	-	Н	7
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Query Match	100.0	39.5	38.2	35.2	34.7	34.2	33.7	33.7	33.2	32.7	32.2	31.7	31.2	31.2	31.2		31.2	31.2	31.2	31.2	31.2	31.2	31.2
Score	199	78	16	70	69	89		67	99	92	64	63	62	62	62	62	62	62	62	62	62	62	62
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### ALIGNMENTS

		P80214;	01-FEB-1994 (REL. 28, CREATED)			BACTERIOCIN	PLNA.	LACTOBACILLUS PLANTARUM.	BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; LACTOBACILLACEAE;			SEQUENCE FROM N.A.			DIEP B.D., HAVARSTEIN L.S., NISSEN-MEYER J., NES F.I.:							STRAIN-C11;	MEDLINE: 96345611.		"Characterization of the locus responsible for the pacteriocin	production in Lactobacillus plantarum C11.";	J. BACTERIOL. 178:4472-4483(1996).	[3]
RE	H	ğ	ជ	ដ	ដ	B	S	os	8	ဗ	Z.	æ	2	X	Æ	R	RT	F	RL	R.	RP	2	X	RA	R	RI	꿊	N.

SEQUENCE OF 26-47. STRAIN=C11;

MEDLINE; 94065628. NISSEN-MEYER J., GRANLY LARSEN A.G., SLETTEN K., DAESCHEL M., NES I.F.;

"Purification and characterization of plantaricin A, a Lactobacillus plantarum bacteriocin whose activity depends on the action of two 

PEPTIGES.";
J. GEN. MICROBIOL. 139:1973-1978(1993).
J. GEN. MICROBIOL. 139:1973-1978(1993).
J. GEN. MICROBIOL. 139:1973-1978(1993).
J. GEN. MICROBIOL. TABLE BACTENED BACTORY.
CLOSELY RELATED LACTORACILLUS SPECIES. IT MAY ACT AS A PORE-FORMING PROTEIN, CREATING A CHANNEL IN THE CELL MEMBRANE TROUGH A "BARREL STAVE" MECHANISM.
J. SUBGNIT: ACTIVE PLANTARICIN A IS COMPOSED OF AN ALPHA CHAIN AND A BETA CHAIN SEQUENCE IS SHOWN.

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modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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"The complete sequence of a 6146 bp fragment of Saccharomyces cerevistae chromosome III contains two new open reading frames."; FRAST 8:569-575(1992).
-!- FUNCTION: REQUIRED FOR EFFICIENT MATING.
-!- INDUCTION: BY MATING PHEROMONES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FIG2 OR YCR089W OR YCR89W OR YCR1102.
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
EUKRARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOMYCETES; SACCHAROMYCETALES;
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Pred. No. 1.20e-02;
8; Mismatches 7; Indels
                                                                                                                                                                                                    BACTERIOCIN PLANTARICIN A.
MISSING (IN THE ALPHA CHAIN).
A6083DE9 CRC32;
                                                                                                                                                                                                                                                      Score 199; DB 1; Lengtn 40,
Pred. No. 5.90e-32;
...ant-hes 0; Indels
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PIR; S25345; S23345.
SGD: 1003312; FIG2
SEQUENCE 1609 AA: 166049 MW; DE974CE8 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-WAY-1992 (REL. 22, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
FACTOR INDUCED GENE 2.
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                                                                                                                                                                                                                                                                                                                                                     1 KSSAYSLQMGATAIKQVKKLFKKWGW 26
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IDUA_CANFA STANDARD; F

QD1634;

01-FEB-1994 (REL. 28, CREATED)
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48
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5458 MW;
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Local Similarity 34.8%;
hes 8; Conservative
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les 26; Consermation
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                                                                                                                    EMBL; X75323; G452406; -. EMBL; X94434; E217591; -. PIR; A45913; A45913. ANTIBIOTIC; BACTERIOCIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  FIG2_YEAST
P25653;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mucopolysaccharidosis I.";
GENOMICS 14:763-768(1992).
-!- CATALYTIC ACTIVITY: HYDROLYSIS OF ALPHA-L-IDURONOSIDIC LINKAGES IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MENON K.P., TIEU P.T., NEUFELD E.F.; "Architecture of the canine IDUA gene and mutation underlying canine mucopolysaccharidosis I.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -1- SUBCELLULAR LOCATION: LYSOSOMAL.
-1- SUBCELLULAR LOCATION: LYSOSOMAL.
-1- TISSUE SPECIFICITY: FOUND UBIQUITOUSLY.
-1- PTM: A SMALLER 63 KDA PROTEIN PROBABLY ARISES FROM IDUA PROTEIN
BY PROTEOLYTIC CLEAVAGE.
-1- DISEASE: DEFECTS IN IDUA ARE THE CAUSE OF MUCOPOLYSACCHARIDOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                       CANIS FAMILIARIS (DOG).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
CARNIVORA; FISSIPEDIA; CANIDAE; CANIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE I (MPS I).
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Pred. No. 2.93e-02;
8; Mismatches 8;
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7358E9D7 CRC32;
01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
ALPHA-L-IDURONIDASE PRECURSOR (EC 3.2.1.76).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; A42420; A42420
PROSITE; PS01027; GIXCOSYL_HYDROL_F39; 1.
PFAM; PF01229; GIXCOSYL_HYDROL,
HYDROLASE; GLYCOSIDASE; LYSOSOME; SIGNAL.
                                                                                                                                                                                                                                               SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
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POTENTIAL.
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EMBL; L01059; -; NOT_ANNOTATED_CDS.
EMBL; L01060; -; NOT_ANNOTATED_CDS.
EMBL; L01061; -; NOT_ANNOTATED_CDS.
EMBL; L01065; G552348; -.
EMBL; M81893; G163964; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   267 SSIYILEQEQATVQQIRRLFPKFA 290
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
TISSUE-TESTIS, AND FIBROBLAST;
MEDLINE; 93052413.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      72939 MW;
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Matches 8; Conservative
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655 AA;
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MEDLINE; 92202199.
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CARBOHYD
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                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN439-80 / SEROTYPE 0:9;
MEDLINE; 91317716.
MICHIELS T., VANOOTEGHEM J.-C., DE ROUVROIT C., CHINA B., GUSTIN A.,
BOUDRY P., CORNELIS G.R.;
"Analysis of virc, an operon involved in the secretion of Yop
proteins by Yersinia enterocolitica.";
J. BACTERIOL. 173:4994-5009(1991).
-!- INDUCTION: AT 37 DEGREES CELSIUS IN THE ABSENCE OF CALCIUM.
--- BELONGS TO AN OPERON INVOLVED IN THE TRANSLOCATION OF YOP PROTEINS
FUNCTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Molecular cloning, sequencing, and physiological characterization of
the gox operon from Bacillus subtilis encoding the aa3-600 quinol
oxidase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
15-UL-1998 (REL. 36, LAST ANNOTATION UPDATE)
GUINOL OXIDASE POLYPETIDE I (EC 1.9.3.-) (QUINOL OXIDASE AA3-600, SUBUNIT QOXB) (OXIDASE AA(3) SUBUNIT 1)
                                                                                                                                                                                                  BACTERIA: PROTEOBACTERIA; GAMMA SUBDIVISION; ENTEROBACTERIACEAE;
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BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SANTANA M., KUNST F., HULLO M.F., RAPOPORT G., DANCHIN A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 70; DB 1; Length 32;
Pred. No. 3.91e-01;
6; Mismatches 5; Indels
                                                              01-APR-1993 (REL. 25, CREATED)
01-RF-1993 (REL. 25, LAST SEQUENCE UPDATE)
01-FER-1995 (REL. 31, LAST ANNOTATION UPDATE)
YOP PROTEINS TRANSLOCATION PROTEIN A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32 AA; 3815 MW; 41DF6051 CRC32;
                             32 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      larity 31.3%;
Conservative
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                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MSQITTKHITVLFRRW 16
                                                                                                                                                             RERSINIA ENTEROCOLITICA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 MGATAIKQVKKLFKKW 24
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STRAIN-168;
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GOXB OR IPA-38D.
                        YSCA_YEREN
Q01242;
                                                                                                                                                                                  PLASMID PYV
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P34956;
                                                                                                                                                                                                                         ERSINIA.
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      RESULT
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                        A GLASER P., KUNGT F., ARNAUD M., COUDART M.P., GONZALES W., AGLASER P., KUNGT F., ARNAUD M., COUDART M. P., GONZALES W., HULLO M.F., IONESCU M., LUBOCHINSKY B., MARCELINO L., MOSZER I., PRESEANE E., SANTHANA M., SCHNEIDER E., SCHWEIZER J., VERTES A.,

RAPOPORT G., DANCHIN A.;

"Bacillus subtilis geneme project: cloning and sequencing of the 97 kb region from 325 degrees to 333 degrees.";

"MOL. MICROBIOL. 10:371-384(1993).

"I. FUNCTION: CATALYZES QUINOL OXIDATION WITH THE CONCOMITANT REDUCTION OF OXYGEN TO WATER. MAJOR COMPONENT FOR ENERGY CONVERSION DURING VEGETATIVE GROWTH.

"I. PATHWAX: TERMINAL STEP IN THE RESPIRATORY CHAIN.

"SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

"I. SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

"I. SUBLIGARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OXIDOREDUCTASE; HEME; COPPER; TRANSMEMBRANE; RESPIRATORY CHAIN; HYDROGEN ION TRANSPORT.
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COPPER B (PROBABLE).
COPPER B (PROBABLE).
COPPER B (PROBABLE).
IRON (HEME A3) (PROBABLE).
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EXTRACELLULAR (POTENTIAL)
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IRON (HEME A) (PROBABLE)
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EMBL; X73124; G413962; -.
EMBL; Z99123; E1186315; -.
PIR; B38129; B38129.
PIR; S39693; S39693.
SUBTILIST; BG10584; QOXB.
PROSITE; PS00077; COXI; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PFAM; PF00115; COX1; 1.
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STRAIN=168;
MEDLINE; 95020537.
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FRANKEL G., CANDY D.C.A., EVEREST P., DOUGAN G.;
"Characterization of the C-terminal domains of intimin-like proteins
"Characterization of the C-terminal domains of intimin-like proteins
of enteropathogenic and enterohemorrhagic Escherichia coli,
citrobacter freundii, and Hafnia alvei.";
INFECT. IMMUN. 62:1835-1842(1994).
-:- FUNCTION: NECESSARY FOR THE PRODUCTION OF ATTACHING AND EFFACING
LESIONS ON TISSUE CULTURE CELLS.
-:- SUBCELLULAR LOCATION: OUTER SURFACE.
                                                                                                                                                                                                                                            MYCOBÄCTĒRIUM LEPRAE.
BACTERIA; FIRMICUTES; ACTINOBACTERIA; ACTINOBACTERIDAE;
ACTINOMYCETALES; CORYNEBACTERINEAE; MYCOBACTERIACEAE; MYCOBACTERIUM.
                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-1996 (REL. 34, CREATED)
01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST NUNCHATION UPDATE)
INTIMIN (OUTER MEMBRANE PROTEIN) (ATTACHING AND EFFACING PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; ENTEROBACTERIACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 68; DB 1; Length 134; Pred. No. 8.97e-01; 8; Mismatches 7; Indels
                                  Length 649;
                                                          8; Indels
IRON (HEME A) (PROBABLE). 7C64B76E CRC32;
                                                                                                                                                                                                                                                                                                      ROBISON K., SMITH D.R.;
SUBMITTED (MAR-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- SIMILARITY: BELONGS TO THE DEDA FAMILY.
                                 Score 69; DB 1; LA
Pred. No. 5.93e-01;
4; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            134 AA; 14249 MW; 7F5164A5 CRC32;
                                                                                                                                                                                01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
HYPOTHETICAL 14.2 KD PROTEIN B1177_C2_172.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           280 AA
                                                                                                                                                          PRT; 134 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91 FPKHFGPGHVALVERLFNRWG 111
          73838 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 YSLOMGATAIKOVKKLFKKWG 25
                                                                                                  22 SIALSTIAIIFVLTYFKKWKW 42
                                 34.7%;
ilarity 42.9%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34.2%;
28.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U00011; G466816; -. HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                           STANDARD;
417 4
649 AA;
                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
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YQO7_MYCLE
Q49642:
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P52869;
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MEDLINE; 93289813.
WEINSTOCK K.G., STRATHERN J.N.;
WOLOCULAR GENETICS IN SACCHATOMYCES kluyver1: the HIS3 homolog and its use as a selectable marker gene in S. kluyver1 and Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SACCHAROWYCES KLUYVERI (YEAST).
EURARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOMYCETES; SACCHAROMYCETALES;
SACCHAROMYCETACEAE; SACCHAROMYCES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                                                                                                                                                                                                         Length 280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Indels
-!- SIMILARITY: BELONGS TO THE EAE/INVASIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUL-1993 (REL. 26, CREATED)
01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)
01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
HYPOTHETICAL PROTEIN IN HISS 3'REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                      Score 67; DB 1; L
Pred. No. 1.35e+00;
6; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    103 107 POLY-SER.
341 AA; 37381 MW; 64772A58 CRC32;
                                                                                                                                                                                                                                                                                                                            NON_TER 1 1 SEQUENCE 280 AA; 30146 MW; FBC2C19D CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 9
ID PPOL SARPE STANCEL.
AC Q11208;
DT 01-OCT-1996 (REL. 34, CREATED)
ht 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT; 341 AA.
                                                                                                                                                                                                                                                                                                                                                                                                            33.7%;
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                                                                                                                                                                                                                                                                   EMBL; L29509; G472359; -. OUTER MEMBRANE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     209 PSSIKELKDLYDDWG 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11 ATAIKQVKKLFKKWG 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                133 SQVKSLRKVFKKW 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YEAST 9:351-361(1993).
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12 TAIKQVKKLFKKW 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; S31236; S31236.
HYPOTHETICAL PROTEIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
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ID YHS3_SACKL
AC Q03000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cerevisiae
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15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -i- SIMILARITY: BELONGS TO THE PARP FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                       MEDINE: 94170813.

MASUTANI M., NOZAKI T., HITOMI Y., IKEJIMA M., NAGASAKI K.,
DE PRATI A.C., KURATA S., NATORI S., SUGIMURA T., ESUMI H.;
Cloning and functional expression of poly(ADP-ribose) polymerase
CDNA from Sarcophaga peregrina.";
EUR. J. BIOCHEM. 220:607-614(1994).
-! FROTISIN: POLY(ADP-RIBOSE] POLYMERASE MODIFIES VARIOUS NUCLEAR
PROTEINS BY POLY(ADP-RIBOSYL)ATION. THE MODIFICATION IS DEPENDENT
ON DNA AND IS INVOLVED IN THE REGULATION OF VARIOUS IMPORTANT
CELLULAR PROCESSES SUCH AS DIFFERENTIATION, PROLIFERATION, AND
TUMOR TRANSFORMATION AND ALSO IN THE REGULATION OF THE MOLECULAR
                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
POLY TADP-RIBOSE] POLYMERASE (CC 2.4.2.30) (PARP) (ADPRT) (NAD(+) ADP-RIBOSYLTRANSFERASE) (POLY (ADP-RIBOSE) SYNTHETASE).
SARCOPHAGA PEREGRINA (FLESH FLY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRANSFERASE; GLYCOSYLTRANSFERASE; NAD; DNA-BINDING; NUCLEAR PROTEIN; ADP-RIBOSYLATION; ZINC-FINGER; ZINC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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NAD-BINDING.
BY SIMILARITY.
NUCLEAR LOCALIZATION SIGNAL 1ST PART.
NUCLEAR LOCALIZATION SIGNAL 2SUD PART.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                               EUKARYOTA; METAZOA; ARTHROPODA; TRACHEATA; HEXAPODA; INSECTA;
PTERYGOTA; DIPTERA; BRACHYCERA; MUSCOMORPHA; OESTROIDEA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C9E71E28 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 66; DB 1; L
Pred. No. 2.02e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; D16482; G538248; -.
PROSITE; PS00347; PARP_ZN_FINGER_1; FALSE_NEG.
PROSITE; PS50064; PARP_ZN_FINGER_2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUL-1989 (REL. 11, CREATED)
15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY
                                                                                                                                          SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE; 94170813.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      552 KNSFYKLQLLESDMKNRFWVFRSWGR 577
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similarity 34.6%;
9; Conservative
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PFAM; PF00644; PARP; 1.
PFAM; PF00645; zf-PARP; 2.
HSSP; P26446; 4PAX.
                                                                                                                       SARCOPHAGIDAE; SARCOPHAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
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19
126
211
232
878
878
896 AA;
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P11009;
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SEQUENCE
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ZN_FING
ZN_FING
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MEDLINE; 96256676.

A FRITZ-WOLF K., SCHNYDER T., WALLIMANN T., KABSCH W.;

RITZ-WOLF K., SCHNYDER T., WALLIMANN T., KABSCH W.;

T "STLUCCHOO SHICKLY OF THE TRANSFER OF PHOSPHATE BETWEEN

TO ATP AND VARIOUS PHOSPHOGENS (E.G. CREATINE PHOSPHATE). CREATINE

TISSUES WITH LARGE, FLUCTUATING ENERGY DEMANDS, SUCH AS SKELETAL

TISSUES WITH LARGE, FLUCTUATING ENERGY DEMANDS, SUCH AS SKELETAL

C HUSCLE, HEART, BRAIN, AND SPERMATOZOA

TO ATALYTIC ACTIVITY: AND THE CHARACTOR OF FOUR WICK HOMODIMERS.

C -- CAPALYTIC ACTIVITY: AND THE CHARACTOR OF FOUR WICK HOMODIMERS.

C -- SUBGINIT: EXISTS AS AN OCTAMER COMPOSED OF FOUR WICK HOMODIMERS.

C -- SUBGINIT: EXISTS AS AN OCTAMER COMPOSED OF FOUR WICK HOMODIMERS.

C -- SUBGINIT: EXISTS AS AN OCTAMER CANDIOLIPIN.

C -- SIMILARIY: THE FOUR DIFFERRNT ISOZYMES OF CREATINE KINASES: B, M,

CC -- TISSUE SPECIFICITY: EXPRESSED IN THE LEG MOSCLE AND HEART.

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TRANSFERASE; KINASE; MULTIGENE FAMILY; MITOCHONDRION; TRANSIT PEPTIDE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE; 88162838.
HOSSIG J.P., SCHLEGEL J., WECMANN G., WYSS M., BOEHLEN P.,
HOSSIG J.P., SCHLEGEL J., MALLIMAN T., PERRIARD J.-C.;
"Distinct tissue specific mitochondrial creatine kinases from chicken brain and striated muscle with a conserved CK framework.";
                                                                                                                                                                                                                                                                                                                                                                                                                            MUCHLEBACH S.M., WIRZ T., BRAENDLE U., PERRIARD J.-C.;
"Evolution of the creative kinases. The chicken acidic type
mitochondrial creatine kinase gene as the first nonmammalian gene.";
J. BIOL. CHEM. 271:11920-11929(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
CREATINE KINASE, SARCOMERIC MITOCHONDRIAL PRÉCURSOR (EC 2.7.3.2) (S-
MTCK) (MIB-CK) (BASIC-TYPE MITOCHONDRIAL CREATINE KINASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                        EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ARCHOSAURIA; AVES;
NEOGNATHAE; GALLIFORMES; PHASIANIDAE; PHASIANINAE; GALLUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 65; DB 1; Length 419;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 21-419 FROM N.A., AND SEQUENCE OF 40-69 IISSUE-SKELETAL MUSCLE, AND HEART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BIOCHEM. BIOPHYS. RES. COMMUN. 151:408-416(1988).
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6; Mismatches 2
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PIR; A27708; A27708.
PBB; 1CK; 07-JUL-97.
PROSITE; PS00112; GUANIDO_KINASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    47084 MW;
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                                                                                                                                                                                                                                                                                                SEQUENCE OF 1-39 FROM N.A.
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                                                                                                                            GALLUS GALLUS (CHICKEN).
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                                                                                                                                                                                                                                                                                                                                            STRAIN-WHITE LEGHORN; MEDLINE; 96216114.
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419 AA;
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                                  01-FEB-1995 (REL. 31, CREATED)
01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN FEUA-SIGW INTERGENIC REGION
                                                                                                                                                                                              QUIRK P.G., GUFFANTI A.A., CLEJAN S., CHENG J., KRULMICH T.A.; "Isolation of Tn917 insertional mutants of Bacillus subtilis that are resistant to the protonophore carbonyl cyanide
                                                                                                                                                                                                                                                                                   STRAIN-168;
LIU H., HAGA K., YASUMOTO K., OHASHI Y., YOSHIKAWA H., TAKAHASHI H.;
SUBMITIED (APR-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- SIMILARIIY: BELONGS TO THE ARAC/XYLS FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                      BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00041; HTH_ARAC_FAMILY_1; 1.
PROSITE: PS01124; HTH_ARAC_FAMILY_2; 1.
PFAM: PP00165; HTH_2; 1.
HYPOTHETICAL PROTEIN; TRANSCRIPTION REGULATION; DNA-BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        201 H-T-H MOTIF (BY SIMILARITY).
60763 MW; 4CD7344C CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 64; DB 1; Length 529;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIINE; 92295566.
TELFORD E.A.R., WATSON M.S., MCBRIDE K., DAVISON A.J.;
"The DNA sequence of equine herpesvirus-1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EQUINE HERPESVIRUS TYPE 1 (STRAIN AB4P) (EHV-1).
VIRUSES; DSDNA VIRUSES, NO RNA STAGE; HERPESVIRIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-DEC-1992 (REL. 24, CREATED)
01-DEC-1992 (REL. 24, LAST SEQUENCE UPDATE)
01-DEC-1992 (REL. 24, LAST ANNOTATION UPDATE)
MAJOR CAPSID PROTEIN (MCP) (CAPSID PROTEIN VP5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 4.48e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Mismatches
            529 AA.
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                                                                                                                                                                                                                                  m-chlorophenylhydrazone.";
BIOCHIM. BIOPHYS. ACTA 1186:27-34(1994).
              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALPHAHERPESVIRINAE; VARICELLOVIRUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL, L19954; G438457; -.
EMBL; AB002150; D1020256; -.
EMBL, Z99104; E1182097; -.
SUBTLILET; BG10834; YBBB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8 OMGATAIKOVKKLFKKW 24
            STANDARD;
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                                                                                                                                                                     MEDLINE; 94281248.
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                                                                                                           SACILLUS SUBTILIS.
                                                                                                                                                                                                                                                                                                                                   REGULATORS
           YBBB_BACSU
P40408;
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P28920;
                                                                                                                                     BACILLUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA_BIND
SEQUENCE
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
HYPOTHETICAL 12.0 KD PROTEIN IN TUB1-CPR3 INTERGENIC REGION PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
EUKARYOTA: FUNGI; ASCOMYCOTA: HEMIASCOMYCETES; SACCHAROMYCETALES;
SACCHAROMYCETACEAE; SACCHAROMYCES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTAL_RAT STANDARD; PRT; 221 AA.
P00502;
21-JUL-1986 (REL. 01, CREATED)
01-AUG-1988 (REL. 08, LAST SEQUENCE UPDATE)
01-NOY-1995 (REL. 32, LAST ANNOTATION UPDATE)
GLUTATHIONE S-TRANSFERASE YA (EC 2.5.1.18) (LIGANDIN) (CHAIN 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
VIROLOGY 189:304-316(1992).
-!- FUNCTION: MAJOR PROTEIN OF THE ICOSAHEDRAL CAPSID.
-!- SIMILARITY: TO OTHER HERPESVIRUSES MAJOR CAPSID PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1376;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HYPOTHETICAL PROTEIN YML084W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   // Match
31.2%; Score 62; DB 1; Length 102;
Local Similarity 42.9%; Pred. No. 9.73e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENTLES S., BOWMAN S., BARRELL B.G., RAJANDREAM M.A.; SUBMITTED (NOV-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                      1376 AA; 152182 MW; E6F464C0 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 63; DB 1; LA
Pred. No. 6.62e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         102 AA; 12030 MW; 94F162C2 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                102 AA.
                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              487 GAYVILPPAGILLDQMRRFFERW 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 SAY-SLOMGATAIKQVKKLFKKW 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; 246660; G575719; -. HYPOTHETICAL PROTEIN; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53 RSSYYSLTINGSTISLLKKYF 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7; Conservative
                                                                                                                                                                                                                                                                                                                                                             EMBL; M86664; G330835; -. PIR; H36799; VCBED6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-S288C / AB972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                          COAT PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YMI4_YEAST
Q04521;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                              IN ADDITION TO ITS ENZYMATIC ACTIVITY, THE HOMODIMER OF YA CHAINS, CALLED LIGANDIN, BINDS VARIOUS ORGANIC ANIONS, XENOBIOTICS, AND AZOCARCINOGEN DYES. IT ISA CYTOSOLIC PROTEIN FOUND IN MANY MAMMALIAN TISSUES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                   KALINYAK J.E., TAYLOR J.M.; "Rat glutathione S-transferase. Cloning of double-stranded cDNA and induction of its mRNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-FEB-1995 (REL. 31, CREATED)
01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
HEAT SHOCK FACTOR PROTEIN HSF8 (HEAT SHOCK TRANSCRIPTION FACTOR 8)
(HSTF 8) (HEAT STRESS TRANSCRIPTION FACTOR).
                                                                        LAI H.-C.J., LI N.-Q., WEISS M.J., REDDY C.C., TU C.-P.D.;
"The nucleotide sequence of a rat liver glutathione S-transferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
          RATTUS NORVEGICUS (RAT).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
                                                                                                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: BELONGS TO THE GST SUPERFAMILY. ALPHA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 62; DB 1; Length 221;
Pred. No. 9.73e+00;
3; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                K -> R (IN PIR DATA BANK).
; C115D4C3 CRC32;
                               RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; RATTUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            527 AA.
 (CLASS-ALPHA) (CLONES PGST94 & PGTR261).
                                                                                                                                                                                                                                                                                                                                                   CLOSELY RELATED MULTIGENE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                 subunit cDNA clone.";
J. BIOL. CHEM. 259:5536-5542(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PFAM, PF00043, gluts, 1.
HSSP, P08263, 1GSF.
TRANSFERASE, MULTIGENE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           221 AA; 25480 MW;
                                                                                                                               SEQUENCE OF 45-196 FROM N.A. MEDLINE; 82075944.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 43.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           205 LPMDAKQIEEARKIFK 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; K01931; G204495; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 LOMGATAIKQVKKLFK 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  151
                                                      SEQUENCE FROM N.A. MEDLINE; 84185691.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSF8_LYCPE
P41153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A0059
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                                                                                                                                                                                        SCHARE K.D., ROSE S., THIERFELDER J., NOVER L.;
"TWO CDRAS for tomato heat stress transcription factors.";
PLANT PHYSIOL, 102:1355-1356(1993).
-!- FUNCTION: DNA-BINDING PROTEIN THAT SPECIFICALLY BINDS HEAT SHOCK
PROMOTER ELEMENTS (HSE) AND ACTIVATES TRANSCRIPTION (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                 EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS;
ASTERIDAE; SOLANANAE; SOLANALES; SOLANACEAE; SOLANUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRANSCRIPTION REGULATION; NUCLEAR PROTEIN; DNA-BINDING; ACTIVATOR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 62; DB 1; Length 527;
Pred. No. 9.73e+00;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                    -1- SUBUNIT: HÓMOTRIMER.
-1- SUBCELLULAR LOCATION: NUCLEAR.
-1- PIM: EXHIBITS TEMPERATURE-DEPENDENT PHOSPHORYLATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34DE58C9 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PHOSPHORYLATION; HEAT SHOCK; MULTIGENE FAMILY.
DNA_BIND 39 133 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -! - SIMILARITY: BELONGS TO THE HSF FAMILY.
LYCOPERSICON PERUVIANUM (PERUVIAN TOMATO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POLY-GLN.
POLY-GLN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; S25481; S25481.
PROSITE: PS00434; HSF_DOMAIN; 1.
PFAM; PF00447; HSF_DNA-bind; 1.
HSSP; P22121; 3HSF_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           139 143 PA
195 198 PA
527 AA; 57519 MW;
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143
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                                                                                                                     [1]
SEQUENCE FROM N.A.
MEDLINE; 94105354.
                                                                                                                                                                                                                                                                                                                                           SIMILARITY)
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protein - protein database search, using Smith-Waterman algorithm Wed Sep 15 10:39:22 1999; MasPar time 5.79 Seconds 245.104 Million cell updates/sec Run on:

Tabular output not generated.

1 KSSAYSLQMGATAIKQVKKLFKKWGW 26 ) 505-09-068-507A-1 (1-26) from US09068507A.pep Description: Perfect Score: Sequence:

PAM 150 Gap 15 Scoring table:

179066 seqs, 54579741 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

1:sp\_archea 2:sp\_bacteria 3:sp\_fung1 4:sp\_human 5:sp\_invertebrate 6:sp\_mamma1 7:sp\_mhc 8:sp\_organelle 9:sp\_phage 10:sp\_plant 11:sp\_rodent 12:sp\_unclassified 13:sp\_vertebrate 14:sp\_virus sptremb19 Database:

Mean 30.932; Variance 45.599; scale 0.678 Statistics:

SUMMARIES

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### 3.26e+00 4.80e+00 4.80e+00 4.80e+00 4.40e-01 1.48e+00 1.48e+00 2.20e+00 2.20e+00 3.26e+00 3.26e+00 3.26e+00 3.26e+00 5.45e-02 1.27e-01 1.27e-01 1.27e-01 2.92e-01 Pred. No. C-SRC KINASE. PUTATIVE DISEASE RESIS 157AA LONG HYPOTHETICA HYPOTHETICAL 23.1 KD P PHAGE SPP1 DNA SEQUENC PROTEIN-TYROSINE KINAS PROBABLE MEMBRANE SPAN MYELIN TRANSCRIPTION F VIRION PROTEIN (FRAGME 457AA LONG HYPOTHETICA NUCLEOSIDE TRIPHOSPHAT 650AA LONG HYPOTHETICA GABA-BRIB RECEPTOR. GABA-BRIA RECEPTOR. GLYCOPROTEIN GP14. COSMID C06A8. CEREBRIN-50 Description Q17690 O73786 O48573 059134 008620 066678 049635 037319 054923 844 11 960 11 960 11 218 5 450 14 1170 10 1170 10 1174 2 256 9 51 13 225 14 646 14 Query Match Length DB 777 755 755 755 67 67 67 67 67 67 67 67 Score Result

ARCHAEA; EURYARCHAEOTA; THERMOCOCCALES; THERMOCOCCACEAE; PYROCOCCUS.

PYROCOCCUS HORIKOSHII.

SEQUENCE FROM N.A. STRAIN-OT3; MEDLINE; 98344137.

01-JAN-1999 (TREMBLREL. 07, LAST SEQUENCE UPDATE) 650AA LONG HYPOTHETICAL PROTEIN.

2 PRELIMINARY; 059134 059134, 01-316-1998 (TREMBLREL. 0 01-3406-1998 (TREMBLREL. 0 01-JAN-1999 (TREMBLREL. 0

PRELIMINARY;

RESULT

650 AA.

4.80e+00 7.05e+00 7.05e+00 1.03e+01	1.03e+01	1.036+01	1.03e+01	1.50e+01	1.50e+01	1.50e+01	1.50e+01	1.506+01	1.306+01	1.506+01	•	1 506+01	1000	1.000	1.000.1	1.000+01	4 -	-		i
COSMID F38E9. F29G9.6 PROTEIN. GAG PROTEIN.	F22E5.1 PROTEIN.	POLLEN-SPECIFIC 1-AMIN	H19NO/.ZB PROTEIN.	F-ABI, MRNA (FRAGMENT).	DNA POLYMERASE (FRAGME	CONSERVED HYPOTHETICAL	⊷		ENOLASE (ENO).		PUTATIVE SERINE PROIDS	T48 MKNA PRECURSOR:	LI RETROPOSON, URFZ MA	LONG INTERSPERSED REFE	-	HYPOTHETICAL 68.8 KD F	POTHETICAL / 0.2 NU	RETROPOSON, ONE 2	LI RETROIRANGFOSON ONE	HEMAGGICA NAMA TOTOGOGOGO
020176 016371 080624	016719	065028	045624	045623	088960	050975	063777	064175	029133	040993	006670	024548	063289	063305	044107	074977	063779	063288	P97692	152680
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	370		1130	1133	220	265	276	340	366	367	397	419	513	556	599	009	646	685	1300	574
33.2 32.7	32.2		32.2	32.2	31./	31.7	31.7	31.7	31.7	31.7	31.7	31.7	31.7	31.7	31.7	31.7	31.7	31.7	31.7	31.2
655 655 655	64	79	64	64	63	9 0	3 %	9 6	63	63	63	63	63	63	93	63	63	63	63	62
21 23	24	2.5	27	28	500	30	33	3 6	) M	, e.	36	37	8	000	V 7	- 4	4.2	43	44	45

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		RODENT I				Gaps		
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	;) (TE)	LIA; EUTHERI	SG 8.0.	plex."; 97).		Score 77; DB 11; Length 822; Pred. No. 5.45e-02; 7; Mismatches 7; Indels		
	DATE UPD	MMA!	<b>3</b>	COM (19	32;	-02;		
¥.	CON	Æ.	μ. <b>Χ</b>	yst 444	CRC.	45e		
822 AA.	ENCE	ATA.	2	38-1	544	, 5. nato		
	EDOU NNNO	rEBR	0 4 4	an e	EFF	77 No Misi		
PRT;	CREATE LAST S	A; VER	Ω Ω	D., ammali A. 94:	W; 38	Score 77; DB 11 Pred. No. 5.45e- 7; Mismatches	751	56
	06, 06, 08,	RDAT		he c	0.2 0.5 0.5 0.5	7 98; 7 69;	WDW -	WGW
PRELIMINARY;	(TREMBLREL. 06, CREATED) (TREMBLREL. 06, LAST SEQUENCE UPDATE) (TREMBLREL. 08, LAST ANNOTATION UPDATE)	REBC15. RAJTUS NORVEGICUS (RAT). EUKARYOTA: METALOA: CHORDATA; VERTEBRATA: MANMALIA; EUTHERIA; RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; RATTUS.	SEQUENCE FROM N.A. SEQUENCE FROM N.A. MEDLINE; 98070770 MEDLINE; 98070770	KEE Y., YOU J.S., HAKONA C.D., FILLINGS. N.T.) SCHELLER R.H.; "Subbnit structure of the mammalian exocyst complex."; "Subbnit structure of The mammalian exocyst (1997).	PROC. NATIONAL ACADA (2827162)	Query Match Best Local Similarity 33.3%; Matches 7; Conservative	731 TLQLAFIDLRQLLDLFMVWDW 751	6 SLOMGATAIKOVKKLFKKWGW 26
	998 998	NORV (A; )	E FR BRAI ; 98	TRES	F032	h Sim	OLAI	OWG.
LT 1 054923	O54923; O1-JUN-1998 O1-JUN-1998 O1-NOV-1998	RSEC15. RATTUS N EUKARYOT SCIUROGN	[1] SEQUENCE FROM N.A. TISSUE-BRAIN; MEDLINE; 98070770.	KEE Y., YOU J.: SCHELLER R.H.; "Subunit struc	EMBL; A SEQUENC	Query Matc Best Local Matches	731 TI	1S 9
RESULT ID O	검점점점	SOSE	R R R X	RA	S S S	QMX	qq	ογ

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KAWARABAYASI Y., SAWADA M., HORIKAWA H., HAIKAWA Y., HINO Y.,
YAMAMOTO S., SEKINE M., BABA S., KOSIGI H., HOSOYAWA A., NAGAI Y.,
SAKAI M., OGUBA K., OTUKA R., NAKAZAWA H., TAKAMIYA M., OHFUKU Y.,
FUNAHASHI T., TANAKA T., KUDOH Y., YAMAZAKI J., KUSHIDA N., OGUCHI A.,
AOKI K., NAKAMURA Y., ROBB T.F., HORIKOSHI K., MASUCHI Y., SHIZUYA H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHÖRDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-TIF (RAI F(SPF)): TISSUE-CORTEX, AND CEREBELLUM;
MEDLINE; 9722131.
KAUDHANN K., HEGGEL K., HEID J., FLOR P.J., BISCHOFF S., MICKEL S.J.,
MCMASTER G., ANGST C., BITTIGER H., FROESTL W., BETTLER B.;
"Expression cloning of Gaba(B) receptors uncovers similarity to
metabolropic glutamate receptors.";
metabolropic glutamate receptors.";
EMBL; Y10370; E311196; ---
PFAM; PF01094; ANF_receptor; 1.
SEQUENCE 844 AA; 95037 MW; 6611F68D CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHÓRDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-TIF(RAI F [SPE]); TISSUE-CORTEX, AND CEREBELLUM;
MEDLINE: 9722131.
RAUPMANN K., HEGGEL K., HEID J., FLOR P.J., BISCHOFF S., MICKEL S.J.,
MCMASTER G., ANGST C., BITTIGER H., FROEGYL W., BETTLER B.;
"Expression cloning of GABA(B) receptors uncovers similarity to metabotropic glutamate receptors.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                    "Complete Sequence and Gene Organization of the Genome of a Hyper-thermophilic Archaebacterium, Pyrococcus horikoshii OT3."; EMBL; AP000006; D1031515; -. SEQUENCE 650 AA; 75553 MW; EDC92EIE CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                      37.7%; Score 75; DB 1; Length 650; Conservative 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
37.7%; Score 75; DB 11; Length 844;
Best Local Similarity 87.5%; Pred. No. 1.27e-01;
Matches 7; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                  LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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LAST ANNOTATION UPDATE)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EUKARYOTA; METAZOA; CHORDATA; VERTEBRAT; SCIUROGNATHI; MURIDAE; MURINAE; RATTUS
                                                                                                                                                                                                                                                                                                                                                                                                                CREATED)
                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUL-1997 (TREMBLREL. 04, CREATED)
01-JUL-1997 (TREMBLREL. 04, LAST SFOI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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01-NOV-1998 (TREMBLREL. 08,
                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RATTUS NORVEGICUS (RAT).
                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1998 (TREMBLREL.
GABA-BRIB RECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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                                                                                                                                                                                                                                                                      615 VKKIKKIFEKWG 626
                                                                                                                                                                                                                                                                                                       14 IKQVKKLFKKWG 25
                                                                                                                                                                                                        Query Match
Best Local Similarity
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BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COLLSON A.,
GRATION M., DERR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
JONES M., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTNING J., LLOYD C., MCMUTRAY A., MORTIMORE B., O'CALLAGHAN M.,
SMALDON N., SMITH A., SONNAAMMER E., STADEN R., SLOWNKEEN R.,
THIERRY-MIEG J., THOMAS K., VANDIN M., VANGHAN K., MATENSTON J.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
"2.2 Mb of Contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;
RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORRABDITIS.
                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1;
                                                                                             Match 37.7%; Score 75; DB 11; Length 960; Local Similarity 87.5%; Pred. No. 1.276-01; es 7; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36.7%; Score 73; DB 14; Length 950; 47.6%; Pred. No. 2.92e-01; Ative 4; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-RACH;
NEUBAUER A., BRAUN B., KAADEN O.R., OSTERRIEDER K.;
SUBMITTED (JAN-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL: PS09377; E2206595; -
PFAM: PF00606; Glycoprotein_B; 1.
SEQUENCE 950 AA; 106568 MW; B2DE30B2 CRC32;
                                                                                                                                                                                                                                                                                                                                                         EQUINE HERPESVIRUS TYPE 1 (EHV-1),
VIRUSES: DSDNA VIRUSES, NO RNA STACE; HERPESVIRIDAE;
ALPHAHERPESVIRINAE; VARICELLOVIRUS
                                                                                                                                                                                                                                                                                01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
                EMBL; Y10369; E311192; 'PFAM; PF00084; Sushi, 2. PFAM; PF01094; ANF_receptor; 1. SEQUENCE 960 AA; 108203 MW; CD3A2D9E CRC32;
                                                                                                                                                                                                                                                              950 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   218 AA.
                                                                                                                                                                                                                                                            PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10; Conservative
                                                                                                                                                                                                                                                       PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NATURE 368:32-38(1994).
                                                                                                                                                          298 KLFEKWGW 305
                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                        19 KLFKKWGW 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE; 94150718.
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                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                    966678;
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Q66678
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                                                                                                                               Matches
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16 QVKKLFKKWGW 26

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SEQUENCE FROM N.A.
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MEDLINE; 98344137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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Q49635
                                                            LT 9
058919
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BUKARYOTA, VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
EUPHYLLOPHYTES; SPERNATOPHYTA; MAGNOLLOPHYTA; EUDICOTYLEDONS; ROSIDAE;
CAPPARALES; BRASSICACEAE; ARABIDOPSIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  XENOPUS LAEVIS (AFRICAN CLAWED FROG).
EUKARYOTA; METAZOA: CHORDATA; VERTEBRATA; AMPHIBIA; BATRACHIA; ANURA;
MESOBATRACHIA; PIPOIDEA; PIPIDAE; XENOPODINAE; XENOPUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-CY. COLUMBEA:
STRAIN-CY. COLUMBEA:
ROUNSLEY S.D., LIN X., KETCHUM K.A., CROSBY M.L., BRANDON R.C.,
SYKES S.M., KAUL S., MASON T.M., KERLAVAGE A.R., ADAMS M.D.,
SYKES S.M., KAUL S., WASON T.M., KERLAVAGE A.R., ADAMS M.D.,
SOMERVILLE C.R., VENTER J.C.;
SOMERVILLE C.R., VENTER D.C.;
ENBL, ACOUST313 G2660663;
ENBL; ACOUST312;
SEQUENCE 1170 AA; 133397 MW; 9B32952B CRC32;
                                                                                                                                                                                                                                                                             Gaps
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34.7%; Score 69; DB 13; Length 450;
Best Local Similarity 41.7%; Pred. No. 1.48e+00;
Matches 10; Conservative 5; Mismatches 9; Indels
                                                                                                                                                                                                                         Query Match 36.2%; Score 72; DB 5; Length 218; Best Local Similarity 60.0%; Pred. No. 4.40e-01; Matches 9; Conservative 4; Mismatches 2; Indels Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MURPHY S.M., MORGAN D.O.;
MURPHY S.M., MORGAN D.O.;
EUBLITED (MAR-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
ENBL: 8F052430; 62967840;
SEQUENCE 450 AA; 50807 MW; E9717367 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-1998 (TREMBLREL. 06, CREATED)
01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
01-JUN-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
PUTATIVE DISEASE RESISTANCE PROTEIN.
                                                                                                                                  SUBMITTED (NOV-1995) TO EMBL/GENBANK/DDBJ DATA BANKS. EMBL: U3849; G1055042; -- W. 1ACF80C3 CRC32; SEQUENCE 218 AA; 25556 WW; 1ACF80C3 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-AUG-1998 (TREMBLREL. 07, CREATED)
01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
                                    SUBMITTED (NOV-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT; 1170 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  450 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                            106 IAATSVKQVEKLFOK 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C-SRC KINASE.
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048573;
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                                                                                                                                                                                                                                                                                                                                                              KAWARRBAYSI Y., SAWADA M., HORIKAWA H., HAIKAWA Y., HINO Y.,
YAMAMOTO S., SEKINE M., BABA S., KOSUGI H., HOSOYAWA A., NAGAI Y.,
SAKAI M., OGURA K., OTUKA R., NKKAZAWA H., TAKAMIYA M., OHPUKU Y.,
FUNAHASHI T., TANAKA T., KUDOH Y., YAMAZAKI J., KUSHIDA N., OGUCHI M.,
AOKI K., NAKAMURA Y., ROBB T.F., HORIKOSHI K., MASUCHI Y., SHIZUYA H.,
KIKUCHI H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BACTERIA; FIRMICUTES; ACTINOBACTERIA; ACTINOBACTERIDAE; ACOBACTERIUM ACTINOMYCETALES; CORYNEBACTERINEAE; MYCOBACTERIACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                              ARCHAEA; EURYARCHAEOTA; THERMOCOCCALES; THERMOCOCCACEAE; PYROCOCCUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Complete Sequence and Gene Organization of the Genome of a "Complete Sequence and Gene Organization of the Genome of Byper-thermophilic Archaebacterium, Pyrococcus horikoshii OT3."; Byper-thermophilic Archaebacterium, Pyrococcus horikoshii OT3."; Byh RES. 5:55-76(1989).
EMBL; AP000005; D1031220; ". SEQUENCE 157 AA; 18430 MW; 3A304921 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             / Match 34.2%; Score 68; DB 1; Length 157; Local Similarity 30.0%; Pred. No. 2.20e+00; Local Similarity 7; Mismatches 7; Indels tes 6; Conservative 7; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SENDERNO, SMITH D.R.; SHITH D.R.; SUBMITTED (MAR-1994) TO EMBL/GENBANK/DDBJ DATA BANKS. SUBMITTED (MAR-1994) TO EMBL/GENBANK/DDBJ DATA BANKS. SUBMIT 296601; E321707; SENDL, 1000011; G46608; TKANSWEMBRANE; SIGNAL. BYPOTHETICAL PROTEIN; TKANSWEMBRANE; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEGUENCE FROM N.A.
PARKHILL J., BARRELL B.G., RAJANDREAM M.A.;
SUBMITTED (JUN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
OLIVER K., HARRIS D.;
SUBMITTED (JUN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLEEL. 08, LAST ANNOTATION UPDATE)
01-NOV-1998 (TREMBLEEL. 08, LAST ANNOTATION UPDATE)
MICCIAGL 23.1 TO PROTEIN.
MICCIAGL 27.7 C B1177_c1_40.
MICCIAGL 27.0 B1177_c1_40.
                                           01-AGG-1998 (TREMBLREL. 07, CREATED)
01-AGG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
01-JAV-1999 (TREMBLREL. 09, LAST ANNOTATION UPDATE)
157AA LONG HYPOTHETICAL PROTEIN.
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157 AA
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      PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            125 SLEIENKLTREERELYKKWS 144
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          PRELIMINARY;
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                                              Gaps
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01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
PHAGE SPPI DNA SEQUENCE CODING FOR PRODUCTS REQUIRED FOR REPLICATION
                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE: 94172631.
PEDRE X., WEISE F., CHAI S., LUEDER G., ALONSO J.C.;
"Analysis of cis and trans acting elements required for the initiation of DNA replication in the Bacillus subtills bacteriophage
                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
ALONSO J.C., LUDER G., STIEGE A.C., CHAI S., WEISE F., TRAUTNER T.A.;
SUBMITTED (JAN-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PREMIORING, 2010,12).

MADISCULAR A.W. KIRSCHNER M.W.;

MADISCULAR CLOHING Of tyrosine kinases in the early Xenopus embryo:
identification of Eck-related genes expressed in cranial neural crest
DEV. DVN. 203:119-140(1995).

DEV. DVN. 203:119-140(1995).

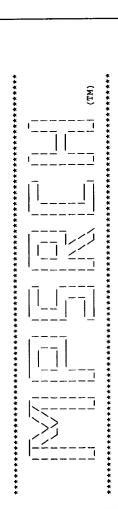
PRAM: PRO0069; pkinase: 1.

TYROSINE-PROTEIN KINASE.
                                                                                                                                                                                                                           BĀCTERIOPHAGE SPP1.
VIRUSES; DSDNA VIRUSES, NO RNA STAGE; TAILED PHAGES; SIPHOVIRIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EUKARYOTA, METAZOA, CHORDATA, VERTEERATA; AMPHIBIA, BAIRACHIA; ANURA;
MESOBATRACHIA, PIPOIDEA, PIPIDAE; XENOPODINAE; XENOPUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
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    34.2%; Score 68; DB 2; Length 214; 28.6%; Pred. No. 2.20e+00; vative 8; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Match
Local Similarity 38.5%; Pred. No. 2.20e+00;
les 5; Conservative 4; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                ALONSO J.C.; SUBMITTED (MAY-1996) TO EMBL/GENBANK/DDBJ DATA BANKS. EMBL; X67865; G439642; EMBL; X97918; E244864; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
PROTEIN-TYROSINE KINASE (G56) (FRAGMENT).
                                                                                                                                       256 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51 AA.
                                                                                                                                      PRT;
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                                                                                                                                                                                                                                                                                                                                                         MOL. BIOL. 236:1324-1340(1994).
                                                91 FPKHFGPGHVALVERLFNRWG 111
                                                                    5 YSLOMGATAIKQVKKLFKKWG 25
                           6; Conservative
                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60 ITSIRELMNRWGW 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14 IKQVKKLFKKWGW 26
                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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Query Match
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Q38150
Q38150;
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                          Matches
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Q91567;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ARCHAEA; EURYARCHAEOTA; THERMOCOCCALES; THERMOCOCCACEAE; PYROCOCCUS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                  REMOND M., SHELDRICK P., LEBRETON F., NARDEUX P., FOULON T.; EMBL; X90443; G1066229; NON_TER 225 225
                                               / Match 33.7%; Score 67; DB 13; Length 51; Local Similarity 41.7%; Pred. No. 3.26e+00; les 10; Conservative 5; Mismatches 9; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                         Length 225;
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Pred. No. 3.26e+00;
3; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 67; DB 1; Length 457;
Pred. No. 3.26e+00;
4; Mismatches 3; Indels
                                                                                                                                                                                         01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
CANINE HERPESVIRUS.
                                                                                                                                                                                                                                                          DSDNA VIRUSES, NO RNA STAGE; HERPESVIRIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07, LAST SEQUENCE UPDATE)
09, LAST ANNOTATION UPDATE)
NON_TER 1 1
NON_TER 51 51
SEQUENCE 51 AA; 5577 MW; 84274507 CRC32;
                                                                                                                                                                                                                                                                                                                                                                SEQUENCE 225 AA; 25754 MW; E3E43F9B CRC32;
                                                                                                                                                                                 225 AA.
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                                                                                                                                                                                PRT;
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01-AUG-1998 (TREMBLREL. 07, LAST SEQ
                                                                                               13 KVSDFGLTKEASAIQDSSKLPVKW 36
                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                      111 AKVYGLQGEMEAVKVADQLFTTW 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        457AA LONG HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 SSAYSLOMGATAIKOVKKLFKKW 24
                                                                                                                                                                                                                                                                                                                                                                                                33.7%;
34.8%;
                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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01-JAN-1999 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PYROCOCCUS HORIKOSHII
                                                                                                                                                                                                                                                         VIRUSES; DSDNA VIRU
ALPHAHERPESVIRINAE.
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                                               Query Match
                                                                                                                                                             LT 13
Q66072
Q66072;
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                                                                    Matches
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058328
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REPAIREL 05, CREATED)
RID 037319;
REMBIREL 05, LAST SEQUENCE UPDATE)
DT 01-0AN-1998 (TREMBLREL 05, LAST SEQUENCE UPDATE)
ROLLONO-1998 (TREMBLREL 05, LAST SEQUENCE UPDATE)
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RASINGARINA A. OSBORRE N.J., DALL D.J.;
RASINGARINA A. OSBORRE N.J., DALL D.J.;
RASINGARINA A. OSBORRE N.J., DALL D.J.;
RASINGARINA A. OSBORRE N.J., DALL D.J.;
RASINGARINA A. OSBORRE N.J., DALL D.J.;
RASINGARINA A. OSBORRE N.J., DR. RESULT PHOSPHATE.
RASINGARINA A. OSBORRE N.J., DR. RESULT PHOSPHATE.
RASINGARIA ROLLOSSE.
RASINGARINA A. OSBORRE N.J., DR. RESULT PHOSPHATE.
RASINGARINA A. OSBORRE N.J., DR. LASINGARINA A. OSBORRE N.J., DR. RE
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n.a. - n.a. database search, using Smith-Waterman algorithm MPsrch\_nn Wed Sep 15 10:38:16 1999; MasPar time 262.06 Seconds 1205.840 Million cell updates/sec Run on:

Tabular output not generated.

1 ATGATGATATTTAAAAAACT........AAATTTTTACCCATCGTTAA 114 TACTACTATAAAATTTTTTGA......TTTAAAAATGGGTAGCAATT >US-09-068-507A-2 (1-114) from US09068507A.seq 114 Description: Perfect Score: N.A. Sequence:

TABLE default Gap 6 Scoring table:

Dbase 0; Query 0 STD : Nmatch Minimum Match 0% Listing first 45 summaries Post-processing:

646147 seqs, 1385953633 bases  $\times$  2

Searched:

Database:

1:em\_bal 2:em\_ba2 3:em\_fun 4:em\_htg 5:em\_hum1 6:em\_hum2
7:em\_in 8:em\_om 9:em\_or 10:em\_ov 11:em\_pat 12:em\_ph
13:em\_tpl 14:em\_ro 15:em\_sts 16:em\_v1

Database:

17:95 bal 18:95 ba2 19:95 htg1 20:95 htg2 21:95 in1 22:95 in2 23:95 om 24:95 ov 25:95 pat 26:95 ph 27:95 pl1 28:95 pl2 29:95 pr1 30:95 pr2 31:95 pr3 32:95 ro 33:95 st 34:95 sts 35:95 sy 36:95 un 37:95 vi

Mean 9.118; Variance 6.864; scale 1.328

Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	% Query Match Length DB	88	qi	Description	Pred. No.
7	114	100.0	5873	17	AF002276	Lactobacillus sake ind	7.64e-44
7	114	100.0	7597	17	LSSAKACNP	L.sake spiA, sppA, spp	7.64e-44
m	31	27.2	10772	21	AF012089	Drosophila melanogaste	3.81e-02
4	29	25.4	216021	31	HUAC004787	Homo sapiens Chromosom	2.65e-01
r)	29	25.4	216021	31	HUAC004787	Homo sapiens Chromosom	2.65e-01
υ	27	23.7	7218	25	I66494	Sequence 14 from paten	1.76e+00
7	26	22.8	1056	23	MVU87256	Mustela vison GT dinuc	4.43e+00
8	26	22.8		58	CAU72146	Camptotheca acuminata	4.43e+00
0	26	22.8	10772	21	AF012089	Drosophila melanogaste	4.43e+00
10	26	22.8	31933	22	CELY50F7A	Caenorhabditis elegans	4.43e+00
11	26	22.8	(*)	21	CEY43F8A	Caenorhabditis elegans	4.43e+00
c 12	26	22.8	44996	21	CEC36B1	Caenorhabditis elegans	4.43e+00
13	26	22.8	Ů.	13	AC002489	Homo sapiens chromosom	4.43e+00

4.4		٦.	ᅼ.	٦.	1.10e+01	1.10e+01	ᅼ	ᅼ	ᅼ	ᅼ	1.10e+01		•	. 69	•	•	2.69e+01	•	ø.	œ.	2.69e+01	œ.	2.69e+01	œ.	۳.	w.	œ.	Ψ.	9e+	Ψ.	
Homo sapiens BAC clone Plasmodium falciparum	Ε	escal	œ		Ø	itis	Drosophila melanogaste	um fal	ᆽ	1113	gan	Endogone pisiformis 18	pisiformis 1	formis 1	oditis	S	S		Caenorhabditis elegans	Drosophila melanogaste		Caenorhabditis elegans	Human DNA sequence ***	Human DNA sequence fro	Caenorhabditis elegans	ţ2	Caenorhabditis elegans	Plasmodium falciparum	itis el	Caenorhabditis elegans	
AC005094 AC006280	DDU73685	LELDHIGN	AB006625	ဌ	CEM176	CEF13G11	AC005653	AC004710	AC006115	CEY51B9	CEY48E1	AF006509	AF006510	AF006511	CEF02D10	CET27F6	CEF32A11	CELC45G7	CET02D9	AC004300	AC005369	CEAA2	HS124K22	HS879K22	CEY67A10	AC006905	AC006705	AC005505	AC006909	AC006898	
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## ALIGNMENTS

Lactobacillus sake inducing peptide preprotein (sppIP), histidine protein kinase homolog (sppK), response regulator homolog (sppK), sakacin kinase homolog (sppK), response regulator homolog (sppR), sakacin P preprotein (sppA), putative sakacin P immunity protein (sppA) and putative ATP-dependent translocator protein (sppT) genes, complete cds.	ĀF002276 92735685 ĀF002276.1 GI:2735685 Lactobacillus sake.		Induction of bacteriocin production in Lactobacillus sake by a secreted peptide J. Bacteriol. 178 (8), 2232-2237 (1996) 96218690 2 (bases 1 to 5873) Brurberg,M.B., Nes,I.F. and Eijsink,V.G.	Lactobacillus Mol. Microbiol. 26 (2), 347-360 (1997) Mol. Microbiol. 26 (2), 347-360 (1997) 3 (bases 1 to 5873) Brurberg, M.B. and Eijsink, V.G.H. Direct Submission	Submitted (05 MAT.1997) Fight Pathology, the Norwegian Clop Research Institute, Ass 1432, Norway Location/Qualifiers 1. 5873 /. radanism="Lactobacillus sake" /strain="LrH673" /db_xref="taxon:1599"
RESULT 1 LOCUS A DEFINITION L P P S S S S O O O O O O O O O O O O O O	ACCESSION PO NID VERSION PA KEYWORDS SOURCE I	ISM CE RS	TITLE JOURNAL MEDLINE REFERENCE AUTHORS TITLE	SEE	JOURNAL S FEATURES SOURCE

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Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillaceae;
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Tichaczek, P.S., Vogel, R.F. and Hammes, W.P.
Cloning and sequencing of sakP encoding sakacin P, the bacteriocin
produced by Lactobacillus sake LTH 673
Microbiology 140 (Pt 2), 361-367 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ž48542.1 GI:695615
Sakacin P; spiA gene; sppA gene; sppE gene; sppK gene;
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Huhne, K., Axelsson, L., Holck, A. and Krockel, L.
Analysis of the sakacin P gene cluster from Lactobacillus sake
Lb674 and its expression in sakacin-negative Lb. sake strains
Microbiology 142 (Pt 6), 1437-1448 (1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 GGAAATAGTTCTAATTTTATTCATAAGATTAAACAAATTTTACCCATCGTTAA 114
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                4 (bases 1 to 7597)
Huehne, K.
Direct Submission
Submitted (28-FEB-1995) Huehne K., Federal Centre for Meat
Research, Microbiology and Toxicology, E.-C.- Baumann-Strasse 20,
Kulmbach, Bavaria, FRG, D-95326
Location/Qualifiers
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    7597
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439. .444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /transl_table=11
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1920. 226
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1920.
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2813.
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572. .1918
/gene="sppK"
572. .1918
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gene="sppR"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'function = "putative protein conferring immunity to sakacin
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                                                                        /traislation-"MDKEFLESSEFYSARFKNFSTLLIMPIAVLLCLVCIFSFFGKRE
ITIEGGOLTTWKQIPILQASTNSVLKQNYLKEGKFYKKGGTLLYYQNTKNONQKRLL
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EGKINQISVSPTVINGSSYTIIGLATISNNNRKLLHYGMTGKIAIITGKTTFFNYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AF012089 10772 bp DNA INV 05-AUG-1997
Drosophila melanogaster cysteine proteinase-1 (CP1) gene, complete
cds, and phenylalanyl tRNA synthetase gene, partial cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 4546 to 4553)
Gray, Y.H., Tanaka, M.M. and Sved, J.A.
P-element-induced recombination in Drosophila melanogaster: hybrid
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Gray, Y. H. M., Sved, J. A., Preston, C.R. and Engels, W.R.

Direct Submission

Submitted (30-JUN-1997) School of Biological Sciences, University of Sydney, Biology All2, Sydney University, NSW 2006, Australia

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                         Drosophija melanogaster
Eukaryotae, mitochodizal alekaryotes; Metazoa; Arthropoda;
Tracheata; Hexapoda; Insecta; Pteryota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gray, Y.H.M., Sved, J.A., Preston, C.R. and Engels, W.R. Structure of the cysteine proteinase (CP1) gene of Drosophila melanogaster and associated mutational effects
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Drosophila melanogaster"
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                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                              Length 7597;
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Pred. No. 7.64e-44;
0; Mismatches 0; Indels
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AF012089.1 GI:2305220
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2310.
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/gene="CP1"
872. .1000
/gene="CP1"
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Best Local Similarity 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HFRKSGVLVSLSEQNLVDCSTKYGNNGCNGGLMDNAFRYIKDNGGIDTEKSYPYEAID
DSCHFNKGTVGATDRGFTDIPQGDEKKMAEAVATVGPVSVAIDASHESFQFYSEGVYN
EPQCDAQNLDHGVLVVGFGTDESGEDYWLVKNSWGTTWGDKGFIKMLRNKENQCGIAS
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Homo saplens Chromosome 16 BAC clone CIT9875K-A-952F10, complete
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Join(2328. .2426,6476. .6690,6751. .7462)
/gene="CPl"
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Pred. No. 3.81e-02;
52; Mismatches 32; Indels
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/db_xref="GI:230522"
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join(8110. .9300,9370. .>9532)
/note="potential orf"
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                                                                                                                                                                                            /product="cysteine proteinase-1"
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4546. /FI"
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6476. .6690
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/gene="CP1"
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/gene-"CP1"
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Best Local Similarity 16.7%;
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ORGANISM

REFERENCE AUTHORS AUTHORS TITLE JOURNAL

REFERENCE AUTHORS JOURNAL

COMMENT

JOURNAL REFERENCE

TITLE

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Address all correspondence version replaced gi:3241936.

Medical Center Dr., Rockville, MD 20850, USA
On Jul 24, 1998 this sequence version replaced gi:3241936.

Address all correspondence to: Mark Adams The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA e-mail address: humgenGtigr.org. The orientation of the sequence is from methods including: XGRAIL (available by anonymous ftp from arthur.epm.ornl.gov), Genes were identified by a combination of five mathor; pencing address: humgenGtigr.org. The orientation of the sequence against Genes were identified by a combination of five arthur.epm.ornl.gov), Genefinder (Phil Green, University of Washington), Genscan (Chris Burge, http://gnomic.stanford.Edu/-chris/GENGCANW.html)searches of the complete sequence against a peptide database, and the human gene Index database at TIGR (http://www.tigr.org/tdb/hgi/hdi.html). Genes without pepetide homolgy having spliced EST hits are termed 'Unknown gene product'. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, http://genome.wustl.edu/eddy/tRNAscan-SE/).
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/note="7608, STS1-cSRL-2491-uA/cSRL-2491-u2, Chr. -, Homo
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                                HUAC004787 216021 bp DNA PRI 24-JUL-1998
Homo sapiens Chromosome 16 BAC clone CIT9875K-A-952F10, complete
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                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 216021)

Adams, M.D., Loftus, B.J., Zhou, L., Crosby, M., Fuhrmann, J., Mason, T.M., Brandon, R., Kim, U.J., Kerlavage, A.R. and Venter, J.C. Homo saplens Chromosome 16 BAC clone CIT987SK-A-952F10
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175810. 175945
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199463. 199572
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Pred. No. 2.65e-01;
48; Mismatches 34; Indels 0;
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60960 a 51778 c 49172 g 53987 t
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Adams, M.D. and Loftus, B.J.
Direct Submission
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Adams, M.D. and Loftus, B.J.
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/clone="A-952F10"
27765. .27872
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Best Local Similarity 15.5%;
Matches 15; Conservative
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RESULT
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Submitted (24-JUL-1998) The Institute for Genomic Research, 9712

Nedical Center Dr., Rockville, MD 20850, USA

On Jul 24, 1998 this sequence version replaced g1:3241936.

Address all correspondence to: Mark Adams The Institute for Genomic Research 9712 Medical Center Dr. Rockville, MD 20850, USA e-mail address: humgen@tigr.org The orientation of the sequence is from spe end to T7 end. Genes were identified by a combination of five methods including: XGRAIL (available by anonymous ftp from arthur.epm.ornl.gov) Genefinder (Phil Green, University of Washington), Genscan (Chris/GENSCANW.html)searches of the complete sequence against a peptide database, and the Human gene Index database at TIGR (http://www.tigr.org/tdb/hgi/hgi.html).

Genes without peptide homolgy having spliced EST hits are termed 'Unknown gene product'. Genes encoding tRNAs are predicted by Location/Qualifiers are reconsidered and product'. Genes encoding tRNAs are predicted by Location/Qualifiers are research.
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/note="7608, STS1-cSRL-24g1-uA/cSRL-24g1-uZ, Chr. -, Homo
                                                                                                                                                                                                                                                                                                                                                                  Submitted (02-JUN-1998) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA, Email:
                  Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo.

1 (bases 1 to 216(Dis.)
Adams, M.D., Loftus, B.J., Zhou, L., Crosby, M., Fuhrmann, J., Mason, T.M., Brandon, R., Kim, U.J., Kerlavage, A.R. and Venter, J.C. Unpublished
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/note="7766, STS1-cSRL-27g3-uA/cSRL-27g3-uZ, Chr.
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Pred. No. 2.65e-01;
40; Mismatches 15; Indels 1;
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51778 c 49172 g 53987 t
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/db_xref="taxon:9606"
/chromosome="16"
/map="#1621-22"
/clone="A-952F10"
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                                                                                                                                                                                                                                                            2 (bases 1 to 216021)
Adams, M.D. and Loftus, B.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 216021)
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Best Local Similarity 15.2%;
Matches 10; Conservative
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645 DKSHCKSKRKYKWMDRYHBCKSMCAMVRGKWSAGTGCMARGWRTWD-SSCTSTKGARR-R 702
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(a. Chases I to 1056)

Brusgaard, K., Shukri, N.M., Malchenko, S., Koroleva, I. and Lohi, O. Direct Submission

Submitted (27-JNN-1997) Breeding and Genetics, Danish Institute of Animal Science, Blichersalle K25, Tjele 8830, DK

Location/Qualifiers

1. 1056
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1482 YYYCYYYYYYYCMGRAMMAAAWYYKRRSCMAWYYYMRGRARKTYYYMARRRGCARSYKK 1541
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                            97 ITTGTTTAATCTTATGAATAAAATTAGAACTATTTCCTGCCATACCACCGTTTATTTTT 38
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Pred. No. 4.43e+00;
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Mustela vison GT dinucleotide repeat, chromosome 1q.
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Pred. No. 1.76e+00;
41; Mismatches 16; Indels
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Patent: US 5670367-A 14 23-SEP-1997;
Location/Qualifiers
                                                                                                                                                       PAT
                                                           1542 YMAMYWAAWTTWCAAAAMAAMYTTYYWMMWYYKKWMY 1578
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Sequence 14 from patent US 5670367.
166494
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/db_xref="taxon:9667"
/chromosome="1"
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complement(300. 320)
/standard_name="1167R"
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1491 c 1486 a
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U87256.1 GI:4099442
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Best Local Similarity 15.9%;
Matches 18; Conservative
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I66494.1
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Nysoideae; Camptotheca.

1 (bases i to 7430)

Maldonado-Mendoza.I.E. Vincent.R.M. and Nessler.C.L.
Molecular characterization of three differentially expressed
members of the Camptotheca acuminata 3-hydroxy-3-methylglutaryl CoA
reductase (HMGR) gene family
Plant Mol. Biol. 34 (5), 781-790 (1997)
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ISGNECSDKKPAAVNWIEGRGKSYVCESIIKEEVVRKVLKTNVASLVELNMLKNLTGS
AMAGALGGENAHASNIVSAVYIATGQDPAONVESSHCITMMEAVNDGKDLHVSVSMPS
IEVIVGGGTQLASQSACLNLLGVKGASKESPGSNSRLLATIVAGSVLAGELSLMSAIA
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/product="3-hydroxy-3-methylglutaryl coenzyme A reductase"
/protein_id="AAB69727.1"
/db_xref="PID:91763334"
/db_xref="GI:1763234"
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LAGLPLDGFDYESILGQCCEMAVGYVQMAVGIAGPLLLDGREYLVPMATTEGCLVAST
NRGCKAIYASGGATSVILRDGMTRAPVVRFGTAKMSAELKFFLEDPRNFDTLAVVFNK
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LTNGVFFTLFFSVAYFLLHRWREKIRTSTPLHIVTVSELAALISLIASVIYLLGFFGI
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join(2075. .3075,4301. .4482,5287. .5638,6302. .6536)
/EC_number="1.1.1.34"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note-"converts HMGCoA in mevalonate precursor for isoprenoid compounds; HMGR; hmg2; similar to protein encoded by GenBank Accession Number L10390"
1 ATGATGATATTTAAAAAACTTTCAGAAAAAGAATTGCAAAAAAATAAACGGTGGTATGGCA 60
                                                                                                                                                                                                                                                           09-SEP-1997
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                                                                                                                                                                                                                                             CAU72146 7430 bp DNA PLN 09-SEP-199 Camptotheca acuminata 3-hydroxy-3-methylglutaryl coenzyme A reductase gene, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Camptotheca acuminata
Eukaryothae, Viridiplantae, Charophyta/Embryophyta group;
Embryophyta; vascular plants; seed plants; Magnoliophyta;
Magnoliopsida; Cornanae; Cornales; Cornineae; Cornaceee;
                                                               703 KGMYARRKMYGTGAAWASATAYSTGAGTTBWRVTSWKMBKYKKTGMMHHCAWK 755
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Pred. No. 4.438+00;
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/db_xref="taxon:16922"
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Maldonado-Mendoza, I.E. and Nessler, C.L.
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Best Local Similarity 82.5%;
Matches 33; Conservative
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EERFRLKIFNINKHKTAKHNQRFAEGKVSFKLAVNKYADLLHHEFRQLMNGFNYTLHK
QLRAADESFKVYTISPAHYTLÞKSYDWRTKGAYTAVKDQGHGGGGMFSSTGGLEGG
HFRKSGYLVGLSEDWLDGCSFKYGNGCNGGLMDNAFRYIKDNGGIDTEKSYPYEAID
DSCHFNKGTVGATDRGFTDIPQGDEKKMAEAYATVGPVSVALDASHESFOFYSEGYYN
EPQCDAQNLDHGVLVVGFGTDESGEDYWLVKNSWGTTWGDKGFIKMLRNKENQCGIAS
        Drosophila melanogaster cysteine proteinase-1 (CP1) gene, complete cds, and phenylalanyl tRNA synthetase gene, partial cds.
                                                                                                                                                                                Eukaryotae; mitochondrial eukaryotes; Metazoa; Arthropoda; Trachedra; Hexappoda; Insecta; Pterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 4546 to 4553)

2 (Say Y. H., Tanaka, M. M. and Sved, J. A.

P-element-induced recombination in Drosophila melanogaster: hybrid element insertion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      University
                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished

3 (bases 1 to 10772)

Gray, V.H.M., Sved.J.A., Preston,C.R. and Engels,W.R.

Direct Submission
Submitted (30-JUN-1997) School of Biological Sciences, Universion
Sydney, Biology Al2, Sydney University, NSW 2006, Australia Location, Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                   Gray, Y.H.M., Sved, J.A., Preston, C.R. and Engels, W.R. Structure of the cysteine proteinase (CP1) gene of Drosophila melanogaster and associated mutational effects
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. .10772
/organism="Drosophila melanogaster"
/d_xref="taxon:7227"
/oin(872. .1000,2310. .2426,6476. .6690,6751. .7707)
/gene="CP1"
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/gene="CP1"
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872. .7707
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    DNA
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6751
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872. .1000
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PVYTVQONTDNLI.PADHYSRQKSDCYYINQPLI.SAGLIDPRLIVGG
EVYRRDEIDSTHYPVFHQADAVRLVTKDKLFERNPGLEEFEEFWSGTILADPRLILPHP
SSWTKANKLMEFRANKLMEHEMKHULVGLTKDLFGPRIKYRWVDTYPFTQPSGTELE
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GFLSGFSEKDLHNLPRYYRFSHYPQCTNDLSFWLPQDIEUDAGFSPNDFYDLVRSVAG
DWTBOILSLVDKFKHPRKTGKSSVCFRIVYRHMERTLTQAEVNEIHRQIASASVDSFNVQ
DWTBOILSLVDKFKHPRKTGKSSVCFRIVYRHMERTLTQAEVNEIHRQIASASVDSFNVQ
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University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rhabditina, Rhabditoidea, Rhabditidae; Peloderinae; Caenorhabditis,
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Wilson, R., Anscough, R., Anderson, K., Baynes, C., Berks, M.,
Bonfield, J., Burton, J., Connell, M., Copsey, T., Cooper, J.,
Bonfield, J., Cardner, J., Connell, M., Copsey, T., Cooper, J.,
Fulton, L., Gardner, A., Green, P., Hawkins, T., Hillier, L., Jier, M.,
Johnston, L., Jones, M., Kershaw, J., Kirsten, J., Laister, N.,
Latreille, P., Lightning, J., Lloyd, C., McMurray, A., Mortimore, B.,
Callaghan, M., Parsons, J., Percy, C., Rifken, L., Roopra, A.,
Saunders, D., Shownkeen, R., Smaldon, N., Smith, A., Sonnhammer, E.,
Staden, R., Sulston, J., Thierry-Mag, J., Thomas, K., Vaudin, M.,
Wulkinson, Sproat, J. and Wohldman, P., Weinstock, L.,
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Pred. No. 4.43e+00;
33; Mismatches 20; Indels 0; Gaps
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                          /product-"phenylalanyl tRNA synthetase"
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| /note-"potential orf"
| /codon_start-1
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Strong,C., Tin-Wollam,A. and Harper,M.
He sequence of C. elegans cosmid Y50F7A
Unpublished (1999)
3 (bases 1 to 31933)
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Best Local Similarity 19.7%;
Matches 13; Conservative
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Department of Genetics, Washington University, St. Louis, MO 63110, USA, and Sanger Centre, Hinxton Hall Cambridge CBOI IRQ, England e-mail: rw@nematode.wustl.edu and jes@sanger.ac.uk
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This sequence may not be the entire insert of this clone. It may be shorter because we only sequence overlapping sections once, or longer because we provide a small overlap between neighboring submissions. This sequence was finished as follows unless otherwise noted: all regions were double stranded or sequenced with an alternate chemistry; an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone

# NEIGHBORING COSMID INFORMATION:

This is a segment of the YAC Y50F7, sequenced to span the gap between T23F4 and F53A10. The 5' cosmid is T23F4, 200 bp overlap; 3' cosmid is F53A10, 200 bp overlap. Actual start of YAC Y56F7 is at base position 25978 of CELK02E7; actual end is at 12429 of CELF56D12

#### NOTES:

Coding sequences below are predicted from computer analysis, using the program Genefinder(P. Green and L. Hillier, ms in preparation). Location/Qualifiers join(1699. .1814,2520. .2565,3062. .3226)
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/translation="MAVAHSTKVPVPTGEKFFTGIICRWASSSNCPFILPTLCSFSDA SRFKFQEVLEKFQKSMIFFNLKSGIFFQNIFPYFLKLLNYVSENATLMLENFFEKLEK /evidence=not\_experimental /protein\_id="AAD12831.1" /db\_xref="PID:g4226119" /db\_xref="G1:4226119" gene CDS

/codon\_start=1

16223. .30367 /gene="Y50F7A.1" join(16223. .16359, 29919. .30015,30197. .30274,30353. .30367) /gene="Y50F7A.1" /note="contains weak similarity to human LGN protein /translation-"MDWIYSWKDSIFYGMCSCSGSPSYHEKDVPHPHDRLDMPLQLKA YRRNSLNAEGYYRDLERMHERGLFTTGINYNAEKSEDFLNMIERMQSNRLDDQRCEMP (GB:U54999); coded for by C. elegans cDNA CEESH91R /codon\_start-1 /protein\_id-"AAD12830.1" /db\_xref-"PID:94226118" /db\_xref-"GI:4226118"

Score 26; DB 22; Length 31933; Pred. No. 4.43e+00; 0; Mismatches 6; Indels 0 Query Match 22.8%; Best Local Similarity 84.2%; Matches 32; Conservative

4976 g 11421 t

5407 c

10129

BASE COUNT ORIGIN

Db 20084 ATTAAAAAATTTTCAAAAAAAATTCCAAAAAAAA 20121

ö

Gaps

ó

# 9 AITIAAAAACIIICAGAAAAAAAAIIGCAAAAAAAA 46 ò

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bin/display/db=wormacesclass_Sequence sobject=Y43F8A
bin/display/db=wormacesclass_Sequence sobject=Y43F8A
Current sequence finishing criteria for the C. elegans genome sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note.

EXCEPTIONS are indicated by an explicit note.

IMPORTANT: This sequence is NOT necessarily the entire insert of the specified clone. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.

IMPORTANT: This sequence is not the entire insert of clone Y43F8A. It may be shorter because we only sequence overlapping sections once, or longer because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.

The true left end of clone Y43F8 is at 11 in this sequence. The true left end of clone C25F9 is at 120384 in this sequence. The true right end of clone C25F9 is at 38756 in this sequence.
                                                                                                                                                                                                                                                                      Caenorhabditis elegans
Sukaryota: Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditina; Rhabditoidea; Rhabditidae; Caenorhabditis.
1 (bases 1 to 38856)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Coding sequences below are predicted from computer analysis, using predictions from Genefinder (P. Green, U. Washington), and other available information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wilson, R., Anscough, R., Anderson, K., Baynes, C., Berks, M., Wilson, R., Ainscough, R., Connell, M., Copsey, T., Cooper, J., Bonfield, J., Burton, J., Connell, M., Copsey, T., Cooper, J., Coulson, A., Crardner, A., Green, P., Hawkins, T., Hillier, L., Jier, M., Johnston, L., Gardner, A., Kershaw, J., Kirsten, J., Laister, N., Laterille, P., Lighthing, J., Lloyd, C., McMurray, A., Mortimore, B., O'Callaghan, M., Parsons, J., Percy, C., Rifken, L., Roopra, A., Saunders, D., Shownkeen, R., Smaldon, N., Smith, A., Sonnhammer, E., Staden, R., Sulston, J., Thierry-Mieg, J., Thomas, K., Vaudin, M., Waughan, K., Waterston, R., Watson, A., Weinstock, L., Whikinson-Sproat, J. and Wohldman, P.
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                                                        Caenorhabditis elegans cosmid Y43F8A, complete sequence. AL032640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (29-OCT-1998) Louis, MO 63110, USA. E-mail: jes@sanger.ac.uk or rw@nematode.wustl.edu
2 (bases 1 to 38856)
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/db_xref="taxon:6239"
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/qene="Y43F8A.1"
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L Submitted (14-SEP-1996) Louis, MO 63110, USA. E-mail:
Submitted (14-SEP-1996) Louis, MO 63110, USA. E-mail:
Jes@sanger.ac.uk or rw@nematode.wustl.edu

2 (Dases 1 to 44996)
S Wilson, R., Ainscough, R., Anderson, K., Baynes, C., Berks, M.,
Bonfield, J., Burton, J., Coonell, M., Copsey, T., Cooper, J.,
Coulson, A., Craxton, M., Dear, S., Du, Z., Durbin, R., Favello, A.,
Fulton, L., Jones, M., Kershaw, J., Kirsten, J., Laister, N.,
Johnston, L., Jones, M., Kershaw, J., Kirsten, J., Laister, N.,
Latreille, P., Lightning, J., Lloyd, C., McMurray, A., Mortinore, B.,
Saunders, D., Shownkeen, R., Smaldon, N., Smith, A., Sonhhammer, E.,
Staden, R., Sulsten, J., Therry wilegy, J., Thomas, K., Vaudin, M.,
Waughan, K., Waterston, R., Watson, A., Weinstock, L.,
Wilkinson-Sproat, J., and Wohldman, P.
                                                       /translation="MGVYT1IFLYALISSVFFPVFQSLIFYRACITLSNSTEPEIACK
SKETTARDNSVHSMSSVILMASSTGLCVSAFFTSRWYGHLSDVKSRKLAFLIPFIGLF
STETILIOVLYPRLSPYYFTYSEVIGASFFTSRWYGHLSDVKSRKLAFLIPFIGLF
ARLEGTISLGSTYFTSLSSYTFTYSEVIGASFFLVAHFIAFNAVFRNDPEKPDLQEK
CVKRKPFCHGTDLKDKKRPPTSSTNLKTLYFSFACSYFPFIGSTRILFFYLKHRFWGA
EEFGYLKAMNTGMTIMSLALYPFLKNLGITDIRLAIFGLTRSIGRAWYAVAWEGWT
                                                                                                                                                                                                                                                                                                                VFIVVFFEMESKFPATAMRSSIATNVGEHERGLAFSLVAVIEALCNLTSSWVFHLAWP
LSLNVFPQLSFVIMPIIILFAITLMILNMRYLEAPELNPEDLTTSIKKSDDISENVNV
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II; Fibronectin type-III domains; Proteasome A-type subunit; Serine
threonine protein kinase; U4/U6 small nuclear ribonucleoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Caenorhabditis elegans.
Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 44996)
Lennard,N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Coding sequences below are predicted from computer analysis, using predictions from Genefinder (P. Green, U. Washington), and other
                                                                                                                                                                                                                                                                                                                                                                                                                               37699. .37771
/gene="Y43F8A.L1"
/note="A1G His H-tRNA; predicted using tRNAscan-SE-1.11;
preliminary prediction; similar to tRNA-His"
37699. .37771
/gene="Y43F8A.L1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               bin/display?db=wormacesclass=Sequence sobject=C36B1
Current sequence finishing criteria for the C. elegans genome
sequencing consortium are that all bases are either sequenced
unambiguously on both strands, or on a single strand with both a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       For a graphical representation of this sequence and its analysis
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6764 g 12407 t
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Best Local Similarity 86.1%;
Matches 31; Conservative
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24742. .24981,25028. .25159)
/gene="Y43F8A.3"
                                                                                                                                                                                                                                               |oin(16922. 17061,17112. 17207,17256. 17374,18018. 18216,
8259. 18442,19113. 19324,19375. 19582,20065. 20196,
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/gene="r43F8A.4"
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/xt.opervnArtollewrrx"
16922. . . 20371
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VSIDYRLSPETVFPENLLDCEKAIDYFLENSLEKFKTDPKKYILVQDSAGGHLATATA
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GIPLEKAKELVPIVLINGHVKPDYREKIDKLLIYRTIIESTHTYNTTKIPKRWEIVEN
SEAQNLLEKVIFDPNFSPIMRENLENLPKSLIVTCEYDVLRDEGLIYSERLMASGVPT
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VFFNILHIFILLNKSWRRQATNVLIIGIAISDIFYLFYYVEGGTREFLENGIPCKCRP
KKTEFLAYYIWIVTIFKDVFRRVSAFSGVSLALIRYLVMKYGARINIRVYTTSTSWA
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RQISTKFLYIDGVFKIIPPILYPFLAFGLLWELKKARDSRKILMRKGEEHEMVHYTKL
VIFWTIGYFLAETPVGISYFYLAYNMGEDFGIIFLANNITVIFVTFLIINSSIHCFFC
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                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
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.23294,23337. .23487)
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IVTAGWSGSVAVWKREQCAQEIKFTGHSSQAGCARPHPGAFTONDYSSLNVYSCSYDG
TVLLMSLSQESPIGELEQHPQPVSKVKPFPNGHHLATACFDSTWRWYDLTTKKELLYQ
EGHSKSVADVAFHPGSVALTGGHCYGRWADRYGRCIMFLDGHTKEIHSYEWMPNG
YEMITGSSDNSMKVWDLRMRRNTYTMPAHTSVVTRVRADAAGQYLVSASFDCTLKMWS
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/translation="MPYANDRIEVT"
/t
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AHAQOHILIFHFVKKHTSYNTAFFSONMVCGDCEKKLTKIVGVDPYRNKVNRNADGS
GPKTVTTKNRLIGVOKKATIVGAKCKLCKMLIHQPGSHYCSTCAYOKGICAMCGKKIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="SPTREMBL:093340"
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VKKTQYLEYFPNNGNMYNCLLYCTMCLDIFSSNSCISDVFNSNIPIWMICIASLMVIQ
                                                                                                                                                                                                                                                                                                                                               /note="similar to DNA directed RNA polymerase II; cDNA EST
EMBL:T00665 comes from this gene; cDNA EST EMBL:T01799
comes from this gene; cDNA EST EMBL:T01866 comes from this
                ATGRGEKPVREYLEEQYSEENTVDEATTLKLVVKSLAQVVPPGSQNIEIAVMKKVNDE
LQORVLSTEEIEALLKVVETERVAAEAEEAASKKR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KGQELNLKAYVKKGFGKEHAKWNPTCGVAFEYDPDNALRHTIYPNVEEWPRSDHSSLP
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21060. .21177,21227. .21384,21441. .21720,21763. .21900,
21967. .22119,22185. .22271))
/gene="C36B1.5"
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/codon_start=1
                                                                                                                                                                     15333. .15455,15510. .15644,15692. .15817,15970. .1
. .16355,16401. .16524,16659. .16865,16912. .16963,
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EMBL:D72539 comes from this gene; cDNA EST EMBL:D75436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            join(18732. 18934,18987. 19033,19065. 19246)
/gene="c3681.6"
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/gene="C35B1.7"
join(22786. .2295
                                                                                                                                                                                                                                                                           17223. .17327)
/gene="C36B1.3"
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/gene="C36B1.6"
                                                                                                                                                /gene="C36B1.3"
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dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note.

IMPORTANT: This sequence is NOT necessarily the entire insert of the specified clone. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.

This sequence is the entire insert of clone C36B1. The true right end of clone F38H1 is at 17998 in this sequence. The start of this sequence (1. 110) overlaps with the end of sequence 281079. The end of this sequence (44893. .44996) overlaps with the start of sequence 296047.
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GVEKKSIPALQDDRTIRKIHMIDDHVMLAFAGLSADARVLVDRARIECQSYKLTLEDP
VTVAYISRYIANTKQRFTQSPGRRPFGISMLIGGFDHDGTPRLFKTEPSGAXYEXVAN
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GOGRESPWSIRDLFLVPETKTVSKFDWFCRLNDTEMCSIHSSPHWKLCSEKHDTYTQR
DAGACPRVQYPSSPAHLITPAINLPDAQRLCLYFRFALLNFHPGQMKVEIFRDGDMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MLLPRHHLGGLLYFCALYLLRASQAQPPTFFALNALPGDSETEV
LAAVKASTANDARVFRACIESLEATGLQROVEIAVPYRLYLDRNFFRQFSLLATI
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TQFALEVVDQTVTFYFRCRRFASRQVTSLPDFSFDEAEKLYIASSAGFIIDNGFEVSLF
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complement(join(13903. .14016,14097. .14393,14440. .14691,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="similar to proteasome A-type submit; cDNA EST EMBL:M79843 comes from this gene; cDNA EST EMBL:D74896 comes from this gene; cDNA EST y8361al.3 comes from this gene; cDNA EST y8361al.5 comes from this gene; cDNA EST y8412d8.3 comes from this gene; cDNA EST from this gene; cDNA EST from this gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(join(7075. .7179,7290. .7366,7941. .8189,
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%gene="c3681.2"
/note="inilar to fibronectin type-III domain"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(join(506. .619,868. .1025,1081. .1154,1
1357. .1466,5816. .5930))
/gene="close1.1"
/note="cDNA EST EMBL:D34750 comes from this gene"
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COMPLement (13993. .15051)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Caenorhabditis elegans"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:6239'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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            //Translation="MREWNLITAMDAEGGIGKNGVLPWRIKKDMQYFASVTKNVSDOS
KRNAVLMGRKCWESIPVTRRPLAGRLNIVLSRQLPAGKSDDYIVVNSLEAAMKLLSEP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          To bases I to 91638)

Hawkins,T.L., Birren,B.W., Fasman,K.H., Nussbaum,C., Lander,E.S., McKernan,K., Munro,C., Richardson,P., Barna,N., Chang,A., Cooke,P., Daly,M.J., Devon,K., Dewar,K., Forrest,C., Gage,D., Geraigery,K., Magos,B., Huang,J., Hul,L., Jacotot,L., Kirby,A., Lane,M., MacKenzie,J., Marquis,N., McDermott,J., Molla,M., Morrow,J., Nachman,A., Naylor,J., Nusbaum,C., O'Connor,T., Olotu,A., Peterson,K., Reeve,M.P., Roberts,D., Rollins,G., Stilwell,J., and Zody,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (22-AUG-1997) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA on Jan 20, 1998 this sequence version replaced gi:2772532. The Staden databases, finishing information, and all chromatographic files used in the assembly of this clone are available from our anonymous ftp site.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Birren, B., Fasman, K., McKernan, K., Nusbaum, C., Richardson, P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalla; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 91638)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens chromosome X, clone 592, WORKING DRAFT SEQUENCE, unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     repeats were identified using RepeatMasker: Smit, A.F.A.
nn, P. (1996–1997)
                                                                                                                                                                                                                                                                                                                                                       Gaps
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*NOTE: This is a 'working draft' sequence. It currently
*consists of 8 contigs. The true order of the places
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* tuns of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                      Score 26; DB 21; Length 44996;
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                                                                                                                                                                                                                                                                                                                          Pred. No. 4.43e+00;
                                                                                                                                                                                                                                                                                                                                                                                           Db 36007 TTATTTGCAATTTTTGCAGAAAGTTTTTAAA 36040
/db_xref="SWISS-PROT:093341"
                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
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Unpublished
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                                                                                                                                                                                                                                                     of annotations omitted.
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HTG; HTGS_PHASE1.
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ilarity 88.2%;
Conservative
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es 30; Conserv
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KEYWORDS
SOURCE
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Direct Submission
Submitted (27-AUG-1998) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Aug 27, 1998 this sequence version replaced gi:3212897.
SUBMITTED BY: WUGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (12-JUN-1998) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NOTICE: This sequence may not represent the entire insert of this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AC005094 158078 bp DNA PRI 27-AUG-1998
Homo sapiens BAC clone RG332B22 from 7p15-p21, complete sequence.
AC005094
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Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primartes; Catarrhini; Hominidae; Homo.
I (bases 1 to 158078)
Edwards,J. and Ozersky,P.
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2 (bases 1 to 158078)
Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 4.43e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 26; DB 19;
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="unknown"
/map="X"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             /chromosome="X"
19091 c 18993
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Washington University
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3 (bases 1 to 158078)
Waterston, R.
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AC005094.1 GI:3478660
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Best Local Similarity 88.2%;
Matches 30; Conservative
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/rpt\_family~"L1"

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such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.
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# MAPPING INFORMATION: The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 mapping project (Exic D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see http://www.nhgri.nih.gov/DIR/GIB/CHR7, send mailto:egreen@nhgri.nih.gov or see http://genome.wustl.edu/gsc

Clone RG32B22 is from the first release of the human BAC library CITB-978SK B. The library contains cloned DNA from the male fibroblast cell line 978SK. See: Shizuya et al., Proc. Natl. Acad. Sci. USA 89:8794-7 (1992); U-J. Kim et al., Genomics 34:213-8 (1996). This clone is available from Research Genetics, Inc. VECTOR: pBeloBAC11 SOURCE INFORMATION:

Selection: chloramphenicol

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NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the right is RG023M10, 200 bp overlap.
Actual start of this clone is at base position 1 of RG332B22;
actual end is at 21981 of RG023M10.
Location/Qualifiers
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5685. :5885 1. 158078
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2877. .13179 rpt\_family-"Alu" 'rpt\_family="L1" 2304. .12600 rpt\_family="L2" 1795. .12068 repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region

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repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region

repeat\_region

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2 (bases I to 198526)
Hyman, R.W., Fung, E.L., Qin, F., Tamaki, T., Kurdi, O.B. and Davis, R.W.
Direct Submission
Direct Submission
Direct Submission
Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           malaria parasite P. falciparum.
Plasmodium falciparum
Eukaryota: Alveolata: Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 198526)
Hyman, R.W., Fung E.L., Qin, F., Tamaki, T., Kurdi, O.B. and Davis, R.W.
Plasmodium falciparum 3D7 chromosome 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACO06280 198526 bp DNA HTG 05-MAR-1999 Lasmodium falciparum 3D7 chromosome 12 PFYAC724 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.
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                                                                                                                                                                                                                                                                                                                                                                           Gaps
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* NOTE: This is a 'working draft' sequence. It currently consists of 9 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Pred. No. 4.43e+00;
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41284. .41544

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4101. .41886

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4225. .42689

/rpt_family="Malk"

4281. .4323

/rpt_family="Malk"

44287. .44415

44788. .44898
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Note: remainder of annotations omitted.
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AC006280.2 GI:4337163
HTG; HTGS_PHASE1.
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Best Local Similarity 79.5%;
Matches 35; Conservative
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DEFINITION
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VERSION
KEYWORDS
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AUTHORS
TITLE
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/Organism="Plasmodium falciparum"
/db_xref="taxon:5833"
/db_xref="taxon:5833"
/chromosome="12"
ORIGIN
Query Match
Best Local Similarity 86.1%; Pred. No. 4.43e+00;
Matches 31; Conservative 0; Mismatches 5: Indels 0; Gaps
Db 65805 AAAAACCTITCAAAAAAAAAAAAC 65840
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Search completed: Wed Sep 15 10:47:20 1999 Job time : 544 secs.

13 AAAAAACTITCAGAAAAAGAATIGCAAAAAAATAAAC 48

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Statistics: Mean 7.049; Variance 6.074; scale 1.161

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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## ALIGNMENTS

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06-0cT-1998 (first entry) Ammalian DNA replication origin consensus sequence, uniorsconsensus. DNA replication origin; mammal; alphaconsensus; uniorsconsensus; anti-gene; DNA replication inhibitor; shuttle vector construct creation;
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bacteria that includes previously unrecognised, strongly regulatable promoter elements (see T67142-48). Expression of genes under the control of such promoters is dependent upon expression of the IF-K-R dene cluster or an analogue. Thus, the expression of a gene under the control of the promoter element in cells that gene under the k and R genes can be induced at will by adding the cognate, synthetic (harmless) inducing peptide. A recombinant vector containing the gene expression system, and host cells transformed with this vector, incorporated in the chromosome, and/or having integrated into its chromosome a promoter linked to an integrated gene encoding a specific protein are claimed. Typical applications are in fermentations (e.g. where the gene for the next the bacteria express a surface antigen, as vaccines. Sequence 114 BP; 50 A; 12 C; 16 G; 36 T;
                                                                                                                                                                                                                                                                                                                                                               1 atgatgatatttaaaaaactttcagaaaagaattgcaaaaaaataaacggtggtatggca 60
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Oligonucleotide probe MK14-A
Oligonucleotide; DNA probe; mycobacteria; disease diagnosis;
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detection and amplification of Mycobacteria nucleic acid in
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Pred. No. 8.34e-03;
39; Mismatches 9; Indels
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26-MAY-1992; US-889651.
(BECT ) BECTON DICKINSON CO.
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Best Local Similarity 0.0%;
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WPI; 93-378844/48
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01-DEC-1993.
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This sequences of the invention, designated uniorsconsensus.

Consensus sequences of the invention, designated uniorsconsensus.

Consensus sequences of the invention, designated uniorsconsensus.

Consensus sequences or an anti-gene (comprising a dual stranded copy of the consensus) is used to inhibit DNA replication of the vitro. The consensus sequences can also be inserted into an expression vector, used subsequently for in vitro transfection of expression vector, used subsequently for in vitro transfection of control initiation of DNA replication. They can also be used used to maintain circular plasmids that are capable of semi-conservative replication in proliferating mammalian cells, or inserted into mammalian or human artificial chromosoma function. The consensus sequence can be constructs therapy. Particularly, they are used to create shuttle vector constructs therapy. Particularly, they are used to create shuttle vector constructs of or defining the essential mammalian elements required for maintenance of corromosomal function. The consensus sequence can be combined with cloned human telomeres and large centrometric blocks for assembly of human artificial chromosomes and maintained as bacterial plasmids, circular or and inear, large or small yeast artificial chromosomes (YACs) or as episomal
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                                                                                                                                              Human or mammalian origin of replication consensus sequences - for inhibiting DNA replication, for controlling initiation of replication, maintaining circular plasmids and in assembly of human artificial chromosomes
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Oligonucleotide probe MK14-A
Oligonucleotide; DNA probe; mycobacteria; disease diagnosis;
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Pred. No. 8.34e-03;
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Q51746 standard; cDNA; 91 BP.
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Best Local Similarity 13.6%;
Matches 12; Conservative
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EP-571911-A.
01-DEC-1993.
24-MAY-1993; 108325.
26-MAY-1992; US-889651.
                                     12-DEC-1997; CA0972.
21-MAY-1997; US-047322.
16-DEC-1996; US-033374.
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Throducing random point mutations into nucleic acods -
by prepo of single stranded template, annealing a primer, elongation,
py prepo of single stranded template, annealing a primer, elongation,
misincorporation, completion of molecules and screening.

Disclosure; p; English.

Random point mutations were introduced into the alpha fragment of
E.coli beta-galactosidase. The wild type sequence was obtained as a
single stranded template and an oligonucleotide was hybridised to
single stranded template and an oligonucleotide was hybridised to
possible nucleotide positions within a specified region. The
variable 3' ends generated in this way are used as primers for
transcriptase and the molecules are completed to forms that can be
amplified and then expressed in a suitable host-vector system.

The sequence covers all 176 difft base substitutions, most of which
see also p80575.

Sequence 204 BP; 21 A; 47 C; 17 G; 11 T; 108 Others;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39; Indels 1; Gaps 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91 thhyrrmrbnvyrdynrsdaaawyccyrrsvkydccynachhddhyvybbbvynvhnhnn 150
                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N81164;
08-NoV-1990 (first entry)
Base substituted E.coli beta-galactosidase alpha-fragment.
E.coli beta galactosidase alpha-fragment; base substitutions; ss.
Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-NOV-1990 (first entry)
asse substituted E.coli beta-galactosidase alpha-fragment.
E.coli beta galactosidase alpha-fragment; base substitutions; ss.
Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47 C; 17 G; 11 T; 108 Others;
    40; Mismatches 10; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lehtovaara P, Knowles J, Koivula A, Bamford J, Reinikainen T;
                                        11 ssvhsyyvvhvvshhhsvhhvvhhvhvvhhvvhhvhhyhvyvsv 60
                                                                       106 GGGTAAAAATITGTITAATCTIATGAAIAAAATIAGAACTATITCCIGCC 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25.4%; Score 29; DB 1; Length 204; 8.0%; Pred. No. 2.10e-02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     151 cncccbnnhvchnvhbnnhrnwayvrhdarrddvhccvch 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67 AGITCIAAITITAITCAIAAGAITAAACAAAITITACCC 106
                                                                                                                                                                                                                                                                                                                                                               /*tag= a
/*taction=multiple cloning site
187.204
/*tag= b
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187..204
/*tag= b
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                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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                                                                                                                                                                           N81164 standard; DNA; 204 BP.
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0; Conservative
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8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-APR-1987; US-034819.
(SUSO) SUOMEN SOKERI OY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-MAR-1988; 105163.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                     misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                          primer_bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                  EP-285123-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-APR-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-MAY-1988
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Matches
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                                                                                                                                                                                Introducing random point mutations into nucleic acods -
by prepn of single stranded template, annealing a primer, elongation,
misincorporation, completion of molecules and screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 29; DB 1; Length 204;
Pred. No. 2.10e-02;
47; Mismatches 42; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                Disclosure; p; English.
Raddom point mutations were introduced into the alpha fragment of E.coli beta-galactosidase. The wild type sequence was obtained as a single stranded template and an oligonuclectide was hybridised to it to generate a popn of DNA molecules which terminate at all possible nucleotide positions within a specified region. The variable 3 ends generated in this way are used as primers for reverse transcriptase. Nucleotides are misincorporated by the transcriptase and the molecules are completed to forms that can be amplified and then expressed in a suitable host-vector system. The sequence covers all 176 difft base substitutions, most of which occurred singularly in any given mutant.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           108 Others;
                                       (SUSO) STOWEN SOKERI OY.
Lehtovaara P, Knowles J, Kolvula A, Bamford J, Reinikainen T;
WPI; 88-279927/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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Pred. No. 5.26e-02;
15; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            147 nhnncncccbnnhvchnvhbnnhrnwayvrhdarrddvh 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40 TITGCAATICTITTCTGAAAGTITTTTAAATATCATCA 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             204 BP; 21 A;
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nes 10; Conservative
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Local Similarity 44.6%;
hes 25; Conservative
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/*tag= a
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03-APR-1987; US-034819.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-MAY-1985; 105750.
17-MAY-1984; GB-012564.
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(SEAR ) SEARLE G D & CO.
Bell LD, Boseley PG, Porter AG;
WPI; 85-311944/50.
17-MAY-1984; GB-012564.
                                                                                                                            P-PSDB; P50022
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   Human or mammalian origin of replication consensus sequences - for inhibiting DNA replication, for controlling initiation of replication, and retaining circular plasmids and in assembly of human prartificial chromosomes

PT artificial chromosomes

Claim 1; Page 42; S4pp; English.

CC chas sequence represents a human or mammalian DNA replication origin consensus sequences of the invention, designated uniorsconsensus.

CC Administration of the consensus sequence or an anti-gene (comprising a Administration of the consensus is used to inhibit DNA replication of in vivo or in vitro. The consensus is used to inhibit DNA replication of compression vector, used subsequently for in vitro transfection of mammalian cells, to control initiation of DNA replication. They can also be used used to maintain circular plasmids that are capable of Semi-conservative replication in proliferating mammalian cells, or semi-conservative replication in proliferating mammalian cells, or inserted into mammalian artificial chromosome vectors for gene therapy. Particularly, they are used to create shuttle vector constructs for defining the essential mammalian elements required for maintenance of cromosomal function. The conserns sequence can be combined with cloned human telomeres and large centromeric blocks for assembly of human artificial chromosomes (TACS) or as episomal elements.
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                                                                                                                                                                                                                       06-0CT-1998 (first entry)
Mammalian DNA replication origin consensus sequence, uniorsconsensus.
DNA replication origin; human; mammal; alphaconsensus; uniorsconsensus; anti-gene; DNA replication inhibitor; shuttle vector construct creation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 mtwaakrawrwwkkdavwwgakrwwkwvwhrassacmdwkaaktwkggwtwarrywkgrk 62
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Local Similarity 12.9%; Pred. No. 1.31e-01;
Les 11; Conservative 50; Mismatches 22; Indels 2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence encoding new modified human beta interferon polypeptides
      Antiviral; cell growth regulator; immune system regulator; antiproliferative; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-JUN-1998.
112-DEC-1997; CA0972.
21-MAY-1997; US-047322.
16-DEC-1996; US-033374.
(UVMC-) UNIV MCGILL.
COSSONS NH, NIELSEN TO, Price GB, Zannis-Hadjopoulos M;
WPI; 98-362770/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 T;
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G;
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C;
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                                                                                                                                                                      V44650 standard; DNA; 91 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1..501
/*tag= a
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17-MAY-1985; 105750.
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                                                                                                                                                                                                                                                                                                                                                                    gene therapy; ss.
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                                                                                                                                                                                                             V44650;
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05-APR-1995 (first entry)
Generic DNA sequence to generate a random TSAR petide library.
TSAR; totally synthetic affinity reagent; synthetic; binding domain;
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New modified human beta interferon polypeptide(s) - prepd. by plasmid transformed bacteria, with improved antiviral, anti-proliferative and immune regulating actions claim 28; Ohart 2a, page 32; Tipp; Bnglish.

Compared with interferon beta prepd. by recombinant methods, the compared with interferon beta prepd. by recombinant methods, the invention are more active and have different affinities for cell surface receptors (allowing selective targetting); they have higher therapeutic index; improved stability against microbial breakdown during synthesis; and better in vivo solubility and stability. They are also easier to recover from incubation mixts. Sequence 501 BP; 107 A; 31 C; 69 G; 80 T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           366 baarmgdtaytayggnmgdathytbcaytayytbaargcnaargattaywnncayt 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-SEP-1991 (first entry)
Sequence encoding new modified human beta interferon polypeptides
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44 TAAACGGTGGTATGGCAGGAAATAGTTCTAATTTTATTCATAAGATTAAACAAATT 99
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Pred. No. 3.21e-01;
16; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22.8%; Score 26; DB 3; Length 501;
41.1%; Pred. No. 3.21e-01;
rative 16; Mismatches 17; Indels
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N50026 standard; DNA; 501 BP.
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les 23; Conservative
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Matches 23; Conservative
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17-MAY-1985; 105750.
17-MAY-1984; GB-012564.
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11-DEC-1985
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                                                                                                   Score 24; DB 12; Length 114;
Pred. No. 1.89e+00;
27; Mismatches 76; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                    106 GGGTAAAAATTTGTTTAATCTTATGAATAAAATTAGAACTATTTCCTGCCATACCACGGT 47
                                                                                                                                                                                                                                                                                                                                                                              Sequence encoding new modified human beta interferon polypeptides
                            /*tag= a
/note= "this sequence represents 'Z'; Z can be a
sequence of 6, 9 or 12 nucleotides (see
comments)"
effector domain; concateneated heterofunctional protein; linker; direct; rapid; detection; screening; treatment; generic; ss.
                                                                                                                                                                                                                                                                                                                                                                                          Antiviral; cell growth regulator; immune system regulator; antiproliferative; ss.
                                                                                                                                                                                                                                                                                                                          46 TTATTTTTGCAATTCTTTTTCTGAAGTTTTTTAAATATCATCAT 1
                                                                                                                                                                                                                                                            detection in a screening process.
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                 Location/Qualifiers
                                                        18-AUG-1994.

01-FEB-1994 U00977.

01-FEB-1993: US-013416.

30-DEC-1993: US-176500.

31-JAN-1994; US-189331.

(UYNC) UNIV NORTH CAROLINA.

FOWIKES DM. KAY BK;

WPI; 94-279739/34.
                                                                                                                                                                                                                                                                                                                                                            N50034 standard; DNA; 498 BP
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Best Local Similarity 2.8%;
Matches 3; Conservative
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04-SEP-1991 (first entry)
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/*tag=
                       55..60
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                       misc_feature
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                                                   W09418318-A
           Synthetic.
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17-MAY-1984; GB-012564.

18 17-MAY-1984; GB-012564.

19 (SEAR IS SEARLE G D & CC.

19 Bell LD, Boseley PG, Porter AG;

19 WI, 85-311944/50.

19 PSDB; P50033.

10 Wew modified human beta interferon polypeptide(s) - prepd. by plasmid transformed bacteria, with improved antiviral, anti-proliferative and immune regulating actions

10 The second of the invention are more active and have different affinities

10 Compared with interferon beta prepd. by recombinant methods, the compared with invention are more active and have different affinities

10 Compared with invention are more active and have different affinities

11 NRS of the invention are more active and have different affinities

12 for cell surface receptors (allowing selective targetting); they have higher therapeutic index; improved stability against microbial content and prepared the preadown during synthesis; and better in vivo solubility and stability. They are also easier to recover from incubation mixts.

12 Sequence 498 BP; 112 A; 30 C; 68 G; 77 T;
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Claim 28; Chart 21, page 41; 71pp; English.
Compared with interferon beta prepd. by recombinant methods, the INFS of the invention are morter active and have different affinities for cell surface receptors (allowing selective targetting); they have higher therapeutic index; improved stability against microbial breakdown during synthesis; and better in vivo solubility and stability. They are also easier to recover from incubation mixts. Sequence 501 Bp; 108 A; 30 C; 72 G; 79 T;
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04-SEP-1991 (first entry)
Sequence encoding new modified human beta interferon polypeptides
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 24; DB 3; Length 498;
Pred. No. 1.89e+00;
16; Mismatches 18; Indels
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17-MAY-1985; 105750.
17-MAY-1984; GB-012564.
(SEAR ) SEARLE G D & CO.
Bell LD, Boseley PG, Porter AG;
WPI; 85-311944/50.
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N50032 standard; DNA; 501 BP.
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Best Local Similarity 39.3%;
Matches 22; Conservative
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04-SEP-1991 (first entry)
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/*tag=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mey by 50032.

New modified human beta interferon polypeptide(s) - prepd. by plasmid transformed bacteria, with improved antiviral, anti-proliferative and immune requiating actions
anti-proliferative and immune requiating actions
Claim 28; Chart 2k, page 42; 71pp; English.
Compared with interferon beta prepd. by recombinant methods, the compared with interferon are more active and have different affinities for cell surface receptors (allowing selective targetting); they have higher therapeutic index; improved stability against microbial breakdown during synthesis; and better in vivo solubility and stability. They are also easier to recover from incubation mixts. Sequence 501 BP; 111 A; 31 C; 68 G; 80 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
Sequence encoding new modified human beta interferon polypeptides
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Sequence encoding new modified human beta interferon polypeptides
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>US-09-068-507A-2 (1-114) from US09068507A.seq 114 Description: Perfect Score:

N.A. Sequence:

1 ATGATGATATTTAAAAACT........AAAITTTACCCAIGGTAA 114
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TABLE default Gap 6 Scoring table:

Dbase 0; Query 0 STD Nmatch

137068 seqs, 35432894 bases x 2 Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

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Statistics:

1:5A\_COMB 2:5B\_COMB 3:5C\_COMB 4:PCT9\_COMB 5:backfiles1 Mean 6.588; Variance 4.618; scale 1.427 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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18.4 5648 4 PCT-US96-0 Sequence 1, Applicatio 5.17.5 215 1 US-08-238- Sequence 5, Applicatio 2.17.5 729 1 US-08-189- Sequence 9, Applicatio 2.17.5 729 3 US-08-189- Sequence 26, Applicatio 2.17.5 965 3 US-08-188- Sequence 26, Applicatio 2.17.5 1670 3 US-08-188- Sequence 5, Applicatio 2.17.5 1670 1 US-08-189- Sequence 10, Applicati		77	18.4	5232	Н	US-07-841-	_	10-019
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17.5 215 1 US-08-238 - Sequence 5, Application 17.5 215 1 US-08-238 - Sequence 5, Application 17.5 129 1 US-08-189 - Sequence 5, Application 17.5 1670 3 US-08-188 - Sequence 22, Application 17.5 1670 3 US-08-188 - Sequence 5, Application 17.5 1670 1 US-08-189 - Sequence 10, Applica		20	17 5	216	٠,		À	9.62e-01
17.5 215 1 US-08-238- Sequence 5, Application 17.5 729 1 US-08-188- Sequence 9, Application 17.5 965 3 US-08-188- Sequence 22, Application 17.5 1670 3 US-08-188- Sequence 5, Application 17.5 1670 1 US-08-188- Sequence 10, Application 17.5 1670 1 US-08-189- Sequence 10,		2	, ,	1 7	4 ,	02-00-238-	'n	2.71e+00
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17.5 65 3 US-08-188- Sequence 26, Applicati 17.5 1670 3 US-08-188- Sequence 5, Applicati 17.5 1670 1 US-08-188- Sequence 5, Applicati 17.5 1670 1 US-08-189- Sequence 10, Application		20	77.5	7.20	r	001		7./ie+00
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17.5 1670 3 US-08-188- Sequence 5, Application 17.5 1670 1 US-08-189- Sequence 10, Application		0 7	C:/T	206	m	US-08-388-	22	2 710400
17.5 1670 1 US-08-189- Sequence 10, Application		20	17.5	1670	m	US-08-188-	<u>'</u>	000
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US-08-188-	US-08-149-	US-08-377-	US-08-149-	US-08-377-	US-08-188-	0-9681-104	TS-08-480-		T-2/40TCC	US-08-440-	US-08-482-	US-08-368-	US-08-482-	10-00-20	- 206 - 208 -	- T80-80-SD	PCT-US92-1	US-07-991-	US-07-991-	10-00-107	101.00.00	PCT-0896-0	US-08-101-	-101-08-11		-680-90-50	US-07-991-	US-08-323-	
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17.5	C: /T:	7.5	17.5	17.5	17.5	17.5	17.5	16.7			7. QT	16.7	16.7	76.7			20.07	15.8	15.8	15.8		0.0	B.CT	15.8	α 	) (	20.01	15.8	
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21	3 6		57		56	c 27		29			7 6	32	33	34	, C							;			43		* 4	C #	

## ALIGNMENTS

COUNTRY: USA
ZIF: 22313-0299
ZIF: 22313-0299
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FTITNG APPLICATION NUMBER: US/07/935,313 Sequence 14, Application US/08232463
Sequence 14, Application US/08232463
Sequence 14, Application US/08232463
GENERAL INFORMATION:
APPLICANT: DORNER, F. APPLICANT: SCHEIFLINGER, F. APPLICANT: FLANER, F. G. TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Roley & Lardner STREET: 1800 biagonal Road, Suite 500 US-08-232-463-14 STANDARD; DNA; UNC; 7218 BP. 30472/114 IMMU APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/COCKET NUMBER: 30472/114 IMMI
TELECOMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEPAX: (703)838-4109
TELEX. (99149)
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS: STREET: 1800 Diag CITY: Alexandria STATE: VA FILING DATE: XXXXXX RESULT 

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RESULT
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                                   IMMEDIATE SOURCE:
CLONE: pTZgpt-F1s
SEQUENCE 7218 BP; 1944 A; 1491 C; 1486 G; 1929 T; 368 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 2183;
                                                                       y Match 23.7%; Score 27; DB 2; Length 7218; Local Similarity 3.4%; Pred. No. 1.41e-03; hes 2; Conservative 41; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 80.6%; Pred. No. 3.36e-01;
Matches 29; Conservative 0; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MAEDIATE SOURCE:
CLONE: 1.5 Kb Clai fragment from fowl pox virus
CLONE: 2183 BP; 736 A; 326 C; 292 G; 829 T; 0 OTHER.
                                                                                                                                                                                                                                                                                                                              COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/993,073
FILING DATE: 19921218
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1882 AAATACTTCTTACTTAATTCATAAATTCAATAAAT 1917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: KOWAICHY, Alan W.
REGISTRATION NUMBER: 31.535
REFERENCE/DOCKET NUMBER: 6159.197-USO2
TELECOMMUNICATION: INFORMATION:
TELEPHONE: 612-332-5300
TELEPHONE: 612-332-9081
                                                                                                                                                                                         Sequence 1, Application US/07993073
Sequence 1, Application US/07993073
Sequence 1, Application US/07993073
Patent No. 5386855
GENERAL INFORMATION:
APPLICANT: Boyle, David B.
APPLICANT: Kumar, Sharad
TITLE OF INVENTION: Pox Virus Vectors
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                            T
US-07-993-073-1 STANDARD; DNA; UNC; 2183 BP
                                                                                                                                                                                                                                                                            ADDRESSEE: Merchant & Gould
STREET: 3100 No. 5368855west Center
CITY: Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 2183 base pairs TYPE: NUCLEIC ACID STRANDEDNESS: Single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA (genomic)
   LENGIH: 7218 base pairs
            TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                  USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                         55402
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                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                             Query Match
                                                                                                                                                                               XXXXXX
                                                                                              Matches
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Gaps
                                                                            Sequence 27, Application PC/TUS9101746
Sequence 27, Application PC/TUS9101746
GENERAL INFORMATION:
APPLICANT: Thompson, Gregory A
APPLICANT: Redué, Vic C
TITLE OF INVENTION: Plant Desaturases-Compositions and Uses
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESSE:
ADDRESSE: Calgene, Inc.
STREET: 1220 Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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19.3%; Score 22; DB 4; Length 3440;
Best Local Similarity 78.9%; Pred. No. 3.36e-01;
Matches 30; Conservative 0; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
SEQUENCE 3440 BP; 1165 A; 668 C; 540 G; 1067 T; 0 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 27, Application US/08471791
Sequence 27, Application US/08471791
Patent No. 5723595
GENERAL INFORMATION:
APPLICANT: Knouf, Vic C
TITLE OF INVENTION: Plant Desaturases-Compositions
                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2306 TITCITITIGAAAITITITITITITIGAAAITITITGAA 2343
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US-08-471-791-27 STANDARD; DNA; UNC; 3440 BP.
T. 3
PCT-US91-01746-27 STANDARD; DNA; UNC; 3440 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: DISKELLE, 3.00 INCN, 1.00
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 6.0.7
SOFTWARE: Microsoftword 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/01746
FILING DATE: 19910314
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/657,373
FILING DATE: 14-NOV-1990
APPLICATION NUMBER: 07/567,373
FILING DATE: 15-MG-1990
APPLICATION NUMBER: 07/494,106
FILING DATE: 16-MAR-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGNE 69-3 WO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: CGNE TELECOMMUNICATION INFORMATION: TELEPHONE: (916) 753-1510 TELEY. (916) 753-1510 TELEX: 350370 GGNE INFORMATION FOR SEQ ID NO: 27: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Lassen, Elizabeth
REGISTRATION NUMBER: 31,845
NAME: BODINA E. SCHERET
REGISTRATION NUMBER: 34,719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGIH: 3440 base pairs
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California
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                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: US
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STREET:
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                                                                                                       ZIP: 95616
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 2.0 MB storage
COMPUTER: Apple Macintosh
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.1
SOFTWARE: MicrosoftWord 5.1 (a) .
GURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,791
FILING DATE: 6-JUNR-95
CLASSIFICATION DATA:
APPLICATION NUMBER: 07/762,762
FILING APPLICATION WHEE
FILING APPLICATION NUMBER: POT/0891/01746
FILING APPLICATION HAA:
APPLICATION NUMBER: POT/US91/01746
FILING DATE: 14-MAR-1991
CLASSIFICATION NUMBER: POT/US91/01746
FILING DATE: 14-MAR-1991
CLASSIFICATION WHEER: 14-MAR-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
19.3%; Score 22; DB 2; Length 3440;
Best Local Similarity 78.9%; Pred. No. 3.36e-01;
Matches 30; Conservative 0; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: genomic DNA
SEQUENCE 3440 BP; 1165 A; 668 C; 540 G; 1067 T; 0 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2306 ITTCTTTTTGAAATTTTTTTTTTTGAAATTTTTTGAA 2343
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Sequence 5, Application PC/TUS9603940
GENERAL INFORMATION:
APPLICANT: Mandel, Gail, Chong, Jayhong A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Lassen, Elizabeth
REGISTRATION NUMBER: 31,845
NAME: Donna E. Scherer
REGISTRATION NUMBER: 34,719
NAME: Carl J. Schwedler
REGISTRATION NUMBER: 36,924
REFERENCE/DOCKET NUMBER: GGNE 69-5
TELEPHONE: (916) 753-6313
TELEPHONE: (916) 753-1510
TELEFAX: (916) 753-1510
TELEFAX: 380370 GGNE
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JT 5
PCT-US96-03940-5 STANDARD; DNA; UNC; 928
                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/615,784
PRIJNG DATE: 14-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/567,373
FILING DATE: 13-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/494,106
FILING DATE: 16-MAR-1990
ATTONREY/AGENT INFORMATION:
TITLE OF INVENTION: and Uses
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
                                         ADDRESSEE: Calgene, Inc. STREET: 1920 Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 3440 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: double
                                                               CITY: Davis
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
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ID PC
AC XX
DT XX
DE SE
CC SE
CC CC
```

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IIBRARY: CDNA
UNDELICATION:
AUBLICATION INFORMATION:
AUTHORS: Chong, Jayhong A., Tapla-Ram!rez Jos , Toledo-
AUTHORS: Aral, Juan, Zheng, Yingcong, Boutros, Michael C., Altschuler,
AUTHORS: Yelena M., Frohman, Michael A., Kraner, Susan D., Mandel, Gail
TITLE: REST: A Mammalian Silencer Protein that Restricts
TITLE: Sodium Channel Gene Expression to Neurons
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                  COMPRY: New Jetsey
COMPRY: New Jetsey
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
COMPUTER: IBM-Compatible
OPERATING SYSTEM: DOS 5.0
SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/03940
FILING DATE: MARCH 23, 1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 18.4%; Score 21; DB 4; Length 928; Best Local Similarity 74.4%; Pred. No. 9.62e-01; Matches 32; Conservative 0; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RELEVANT RESIDUES IN SEQ ID NO: 5:FROM 1 TO 928 SEQUENCE 928 BP; 363 A; 178 C; 182 G; 205 T; 0 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       643 CAGAAATAGAACAAACAAAATAAAAGGGGATGTGGCTGGAAA 685
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Sequence 4, Application PC/TUS9603940
GENERAL INFORMATION:
APPLICANT: Mandel, Gail, Chong, Jayhong A.
TITLE OF INVENTION: REST Protein and DNA
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
TITLE OF INVENTION: REST Protein and DNA NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSE: Dechert Price & Rhoads
STREET: P.O. Box 5218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PCT-US96-03940-4 STANDARD; DNA; UNC; 1090 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Allen Bloom
REGISTRATION NUMBER: 29,135
REFERENCE/DOCKET NUMBER: 317743-101
TELECOMMUNICATION INFORMATION:
TELEFAX: (609) 520-3214
TELEFAX: (609) 520-3259
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 928 base pairs
TYPE: nuclet acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: CDNA to mRNA
HYPOTHETICAL: no
ANTI-SENSE: no
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DATE: March 24, 1995
                                                                                                                                                                    STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Human
CELL LINE: HeLa
IMMEDIATE SOURCE:
LIBRARY: CDNA
                                                                                                                                          Princeton
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VOLUME: 80
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STATE: New Jersey
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      AUTHORS: Chong, Jayhong A., Tapia-Ramirez Jos, Toledo-AUTHORS: Aral, Juan, Zheng, Yingcong, Boutros, Michael C., Altschuler, AUTHORS: Yelena M., Frohman, Michael A., Kraner, Susan D., Mandel, Gail TITLE: REST: A Mammalian Silencer Protein that Restricts
JOURNAL: Cell
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                                                                     ZIP: 08543-5218
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage COMPUTER: IBM-compatible OPERATING SYSTEM: DOS 5.0
SOFTWARE: WORDPERFECT CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/03940
FILING DATE: MARCH 23, 1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 21; DB 4; Length 1090; Pred. No. 9.62e-01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DATE: March 24, 1995
RELEVANT RESIDUES IN SEQ ID NO: 4:FROM 1 TO 1090
SEQUENCE 1090 BP; 433 A; 206 C; 219 G; 232 T; 0 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         702 CAGAAATAGAACAAACAAAATAAAAGGGGATGTGGCTGGAAA 744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23 CAGAAAAAGAATTGCAAAAAATAAACGGTGGTATGGCAGGAAA 65
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Sequence 3, Application PC/TUS9603940
Sequence 3, Application PC/TUS9603940
GENERAL INFORMATION:
APPLICANT: Mandel, Gail, Chong, Jayhong A.
TITLE OF INFURION: REST Protein and DNA
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PCT-US96-03940-3 STANDARD; DNA; UNC; 1407 BP
                                                                                                                                                                                                                                                                       317743-101
ADDRESSEE: Dechert Price & Rhoads
STREET: P.O. Box 5218
CITY: Princeton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Dechert Price & Rhoads
STREET: P.O. Box 5218
CIIY: Princeton
                                                                                                                                                                                                                    ATTORREY AGENT INFORMATION:
NAME: Allen Bloom
REGISTRATION NUMBER: 29,135
REFERENCE/DOCKET NUMBER: 31774
TELECOMMUNICATION INFORMATION:
TELEPHONE: (609) 520-3214
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1090 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: CDNA to mRNA
                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LIBRARY: CDNA PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match 18.4%;
Local Similarity 74.4%;
les 32; Conservative
                                            New Jersey
: USA
                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Human
CELL LINE: HeLa
                                                                                                                                                                                                                                                                                                                                                                                                                                      0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
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JOURNAL: Ce
VOLUME: 80
                                                                                                                                                                                                                                                                                                                                                                                                                                   HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANTI-SENSE:
                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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AUTHORS: Chong, Jayhong A., Tapia-Ramirez Jos , Toledo-AUTHORS: Aral, Juan Zheng, Yingcong, Boutros, Michael C., Altschuler, AUTHORS: Yelena M., Frohman, Michael A., Kraner, Susan D., Mandel, Gail TITLE: REST: A Mammallan Silencer Protein that Restricts
TITLE: Sodium Channel Gene Expression to Neurons
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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COUNTRY: USA
ZIP: 0843-5218
COMPUTER READABLE FORM:
MEDIOM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
COMPUTER: IBM-compatible
OPERATING SYSTEM: DOS 5.0
SOFTWARE: WORDPEfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/03940
FILING DATE: MATCH 23, 1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 21; DB 4; Length 1407;
Pred. No. 9.62e-01;
0; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DATE: March 24, 1995
RELEVANT RESIDUES IN SEQ ID NO: 3:FROM 1 TO 1407
SEQUENCE 1407 BP; 515 A; 276 C; 306 G; 310 T; 0 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1122 CAGAAATAGAACAAAAAAAAAAAAGGGGATGTGGCTGGAAA 1164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23 CAGAAAAAGAATTGCAAAAAATAAACGGTGGTATGGCAGGAAA 65
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Sequence 27, Application PC/TUS9603940
GENERAL INFORMATION:
APPLICANT: Mandel, Gall, Chong, Jayhong A.
TITLE OF INFORMION: REST Protein and DNA
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JT 8
PCT-US96-03940-27 STANDARD; DNA; UNC; 1461 BP
                                                                                                                                                                                                                        ATTORNEY AGENT INFORMATION:
NAME: Allen Bloom
REGISTRATION NUMBER: 29,135
REFERENCE/DOCKET NUMBER: 317743-101
TELECOMMUNICATION INFORMATION:
TELEFAHONE: (609) 520-3214
TELEFAHONE: (609) 520-3259
INFORMATION FOR SEQ 1D NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1407 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Dechert Price & Rhoads
STREET: P.O. Box 5218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: CDNA to mRNA
HYPOTHETICAL: no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Human
CELL LINE: HeLa
IMMEDIATE SOURCE:
LIBRARY: CDNA
PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 74.4%;
Matches 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Princeton
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08543-5218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ANTI-SENSE: no
ORIGINAL SOURCE:
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US-09-068-507A-2.rni

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LIBRARY: CDNA
PUBLICATION INFORMATION:
AUTHORS: Chong, Jayhong A., Tapia-Ramirez Jos , Toledo-
AUTHORS: Aral, Juan, Zheng, Yingcong, Boutros, Michael C., Altschuler,
AUTHORS: Yelena M., Frohman, Michael A., Kraner, Susan D., Mandel, Gail
TITLE: REST: A Mammalian Silencer Protein that Restricts
JUMENAL: Cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              / Match 18.4%; Score 21; DB 4; Length 1791; Local Similarity 74.4%; Pred. No. 9.62e-01; nes 32; Conservative 0; Mismatches 11; Indels
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STRET: Dechert Price & Rhoads
STRET: D. Box 5218
CITY: Princeton
STATE: New Jersey
COUNTR: New Jersey
COUNTR: 08543-5218
COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
OPERATING SYSTEM: DOS 5.0
SOFTWARE: WORDPERFECT
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DATE: March 24, 1995
RELEVANT RESIDUES IN SEQ ID NO: 6:FROM 1 TO 1791
SEQUENCE 1791 BP; 607 A; 395 C; 406 G; 383 T; 0 OTHER.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 10, Application PC/TUS9603940
Sequence 10, Application PC/TUS9603940
GENERAL INFORMATION:
APPLICANT: Mandel, Gail, Chong, Jayhong A.
TITLE OF INVENTION: REST Protein and DNA
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .T 10
PCT-US96-03940-10 STANDARD; DNA; UNC; 3291 BP.
                                               SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/03940
FILLING DATE: MARCH 23, 1995
CLASSIFTCATION:
ATTONNEY/AGENT INFORMATION:
NAME: Allen Bloom
REGISTRATION NUMBER: 29,135
REFERENCE/DOCKET NUMBER: 31743-101
TELEPHONE: (609) 520-3214
TELEPHONE: (609) 520-3214
INFORMATION FOR SEG ID NO: 6: SEQUENCE CHRACTERISTICS:
LENGTH: 1791 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: Application of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the co
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MOLECULE TYPE: CDNA to mRNA
HYPOTHETICAL: no
ANTI-SENSE: no
ORIGINAL SOURCE:
                            OPERATING SYSTEM: DOS 5.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Human
CELL LINE: HeLa
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOURNAL: Cel
VOLUME: 80
ISSUE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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PUBLICATION INFORMATION:
AUTHORS: Chong, Jayhong A., Tapia-Ramirez Jos , Toledo-
AUTHORS: Aral, Juan, Zheng, Yingcong, Boutros, Michael C., Altschuler,
AUTHORS: Yelena M., Frohman, Michael A., Kraner, Susan D., Mandel, Gail
TITLE: REST: A Mammalian Silencer Protein that Restricts
TITLE: Sodium Channel Gene Expression to Neurons
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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Pred. No. 9.62e-01;
0; Mismatches 11; Indels
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage COMPUTER: IBM-compatible
OPERATING SYSTEM: DOS 5.0
SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
RILING DATE: WORCH POS 5.0
FILING DAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DATE: March 24, 1995
RELEVANT RESIDUES IN SEQ ID NO: 26:FROM 1 TO 1461
SEQUENCE 1461 BP; 528 A; 288 C; 326 G; 319 T; 0 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
COMPUTER: IBM-compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1217 CAGAAATAGAACAAACAAAATAAAAGGGGATGTGGCTGGAAA 1259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23 CAGAAAAAGAATTGCAAAAAATAAACGGTGGTATGGCAGGAAA 65
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Sequence 6, Application PC/TUS9603940
GENERAL INFORMATION:
APPLICANT: Mandel, Gail, Chong, Jayhong A.
TITLE OF INVENTION: REST Protein and DNA
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dechert Price & Rhoads
STRETT: P.O. Box 5218
CITT. Princeton
STATE: New Jersey
                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Allen Bloom
REGISTRATION UNBER: 29,135
REFERENCE/DOCKET NUMBER: 21743-101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (609) 520-3214
TELEFAX: (609) 520-3259
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 1461 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .r 9
PCT-US96-03940-6 STANDARD; DNA; UNC; 1791 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: CDNA to mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 74.4%;
Matches 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Human
CELL LINE: HeLa
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HYPOTHETICAL:
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VOLUME: 80
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Ian C. McLeod
REGISTRATION NUMBER: 20,931
REFERENCE/DOCKET NUMBER: MT 4.1-129
TELECOMMUNICATION INFORMATION:
TELEFAX: (517) 347-4103
TELEFAX: (517) 347-4103
TELEFAX: (517) 347-4103
TELEFAX: (517) 347-4103
TELEFAX: (517) 347-4103
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US-07-841-655-1 STANDARD; DNA; UNC; 5595 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN: NRRL-B-18050
INDIVIDUAL ISOLATE: PACL.0
DEVELOPMENTAL STAGE: N/A
                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: Linear
MOLECULE TYPE: Plasmid DNA
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANELLE: N/A
IMMEDIATE SOURCE: N/A
POSITION IN GENOME: N/A
FEATURE:
FILING DATE: 19911231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HAPLOTYPE: N/A
TISSUE TYPE: N/A
CELL TYPE: N/A
CELL LINE: N/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Michigan
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CITY: Okemos
STATE: Michiga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 48864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HYPOTHETICAL:
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Sequence 1, Application US/07635965C
Patent No. 5260212
GENERAL INFORMATION:
APPLICANT: J.D. Marugg, A.M. Ledeboer, P.A. Vandenbergh and J.T. Henderson TITLE OF INVENTION: Cloned Gene Encoding For Bacteriocin From TITLE OF INVENTION: Pediococcus acidilactici NUMBER OF SEQUENCES: I CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LIBRARY: CDNA
PUBLICATION INFORMATION:
AUTHORS: Chong, Jayhong A., Tapia-Ram!rez Jos , Toledo-
AUTHORS: Aral, Juan, Zheng, Yingcong, Boutros, Michael C., Altschuler,
AUTHORS: Yelena M., Frohman, Michael A., Kraner, Susan D., Mandel, Gail
TITLE: REST: A Mammalian Silencer Protein that Restricts
TITLE: Sodium Channel Gene Expression to Neurons
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Pred. No. 9.62e-01;
0; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTAL.

12. 48864
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
COMPUTER: IBM AT
COMPUTER: IBM AT
COMPUTER: IBM AT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DATE: March 24, 1995
RELEVANT RESIDUES IN SEQ ID NO: 10:FROM 1 TO 3291
SEQUENCE 3291 BP; 1091 A; 694 C; 807 G; 699 T; 0 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1337 CAGAAATAGAACAAACAAAATAAAAGGGGATGTGGCTGGAAA 1379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 11
ID US-07-635-965C-1 STANDARD; DNA; UNC; 5595 BP
                                                                      ATTORNEY AGENT INFORMATION:
NAME: Allen Bloom
REGISTRATION NUMBER: 29,135
REFERENCE/DOCKET NUMBER: 317743-101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (609) 520-3214
TELEFEX: (609) 520-3259
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 3291 base pairs
TYPE: nucletc acid
STRANBEDNESS: Gouble
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: ASCII text editor
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/635,965C
APPLICATION NUMBER: PCT/US96/03940 FILING DATE: March 23, 1995 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Ian C. McLeod
STREET: 2190 Commons Parkway
CITY: Okemos
                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: CDNA to mRNA HYPOTHETICAL: no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 74.4%;
Matches 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: Michigan
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Human
CELL LINE: HeLa
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                           ANTI-SENSE: no
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JOURNAL: CE-
VOLUME: 80
ISSUE:
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Sequence 1, Application US/07841655
Sequence 1, Application US/07841655
Sequence 1, Application US/07841655
Sequence 1, Application US/07841655
Sequence 1, Application US/07841655
Sequence 1, Application US/07841655
TILE OF INVENTION: Cloned Gene Encoding For Bacteriocin TITLE OF INVENTION: Cloned Gene Encoding For Bacteriocin TITLE OF INVENTION: From Pediococcus acidilactici NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS: ADDRESSE: 1 ADDRESSE: 1 STREET: 2190 Commons Parkway
FRAGMENT TYPE: N-terminal, internal and C-terminal fragments ORIGINAL SOURCE: ORGANISM: Pediococcus acidilactici
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: bacteriocin encoding DNA
LOCATION: ECORI to Sall
LOCATION: DNA fragment 5.6 kbp.
IDENTIFICATION METHOD: sequencing
O'THER INFORMATION: DNA needed for bacteriocin expression.
PUBLICATION INFORMATION: N/A
SEQUENCE 5555 BP: 1759 A; 1007 C; 1006 G; 1823 T; 0 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
18.4%; Score 21; DB 1; Length 5595;
Best Local Similarity 69.1%; Pred. No. 9.62e-01;
Matches 38; Conservative 0; Mismatches 17; Indels
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AUTHORS: Juan, Zheng, Yingcong, Boutros, Michael C., Altschuler, Yelena AUTHORS: M., Frohman, Michael A., Kraner, Susan D., Mandel, Gail TITLE: REST: A Mammalian Silencer Protein that Restricts
TITLE: Sodium Channel Gene Expression to Neurons
JOURNAL: Cell
                                                                         COMPUTER: New Jersey
COMPUTER: New Jersey
COMPUTER: USA

ZIP: 08543-5218
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKette, 3.50 inch, 1.44 Mb storage
COMPUTER: IBM-Compatible
OPERATING SYSTEM: DOS 5.0
SOFTWARE: WordPerfect
CUBRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/03940
FILING DATE: March 23, 1995
CLASSIFICATION NUMBER: PCT/US96/03940
FILING DATE: March 23, 1995
CLASSIFICATION NUMBER: 29, 135
REFERENCE/POCKET NUMBER: 29, 135
REFERENCE/POCKET NUMBER: 29, 135
REFERENCE/POCKET NUMBER: 29, 135
REFERENCE (609) 520-3214
TELEPHONE: (609) 520-3214
TELEPHONE: (609) 520-3259
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 6648 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DATE: March 24, 1995
RELEVANT RESIDUES IN SEQ ID NO: 1:FROM -1 TO 5648
SEQUENCE 5648 BP; 1747 A; 1098 C; 1294 G; 1507 T; 2 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 18.4%; Score 21; DB 4; Length 5648; Best Local Similarity 74.4%; Pred. No. 9.62e-01; Matches 32; Conservative 0; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chong, Jayhong A., Tapia-Ramirez Jos ,
Toledo-Aral,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1661 CAGAAATAGAACAAACAAAATAAAAGGGGATGTGGCTGGAAA 1703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23 CAGAAAAAGAATTGCAAAAAATAAACGGTGGTATGGCAGGAAA 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 5, Application US/08238163
Sequence 5, Application US/08238163
Patent No. 5569830
GENERAL INFORMATION:
APPLICANT: BENNETT, Alan
APPLICANT: LABAVITCH, John M.
APPLICANT: STOTZ, Henrik
TITLE OF INVENTION: PLANT INHIBITORS OF FUNGAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 14
ID US-08-238-163-5 STANDARD; DNA; UNC; 215 BP.
            ADDRESSEE: Dechert Price & Rhoads STREET: P.O. Box 5218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: CDNA to MRNA
HYPOTHETICAL: no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LIBRARY: CDNA PUBLICATION INFORMATION:
                                                                STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CELL LINE: HeLa
IMMEDIATE SOURCE:
                                               Princeton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANTI-SENSE: no
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JOURNAL: CE
VOLUME: 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ô
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Pred. No. 9.62e-01;
0; Mismatches 17; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1076 ATGAAAAAATTGAAAAATTAACTGAAAAAGAAATGGCCAATATCATTGGTGGTA 1130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: bacteriocin encoding DNA
LOCATION: ECORI to Sali
LOCATION Argament 5.6 kbp.
IDENTIFICATION METHOD: sequencing
OTHER INFORMATION: DNA needed for bacteriocin
OTHER INFORMATION: expression.
PUBLICATION INFORMATION: N/A
SEQUENCE 5595 BP; 1759 A; 1007 C; 1006 G; 1823 T; 0 OTHER.
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FRAGMENT TYPE: N-terminal, internal and C-terminal FRAGMENT TYPE: fragments
ORIGINAL SOURCE:
ORGANISM: PEdiococcus acidilactici
STRAIN: NRRL-B-18050
         COMPUTER REALIZED.

COMPUTER: Diskette, 5.25 inch, 360 Kb COMPUTER: IBM AT OPERATING SYSTEM: MS-DOS 5.00 SOFTWARE: ASCII text editor CURRENT APPLICATION DATA: APPLICATION NUMBER: US/07/841,655 FILING DATE: 19910225 CLASSIFICATION NUMBER: 07/635,965 FILING DATE: December 31, 1990 ATTORNEY/AGENT INFORMATION: NAME: Lan C. McLeod REGISTRATION NUMBER: 20,931 REFERENCE/DOCKET NUMBER: MT 4.1-140 TELEPHONE: (517) 347-4103 TELEPHONE: (517) 347-4103 TELEFA: (517) 347-4103 TELEFA: No. 517552e INFORMATION: SEQUENCE CHARACTERISTICS: CENTRY. 6595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Mandel, Gail, Chong, Jayhong A.
TITLE OF INVENTION: REST Protein and DNA
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T 13
PCT-US96-03940-1 STANDARD; DNA; UNC; 5648
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Sequence 1, Application PC/TUS9603940
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN: NRRL-B-18050
INDIVIDUAL ISOLATE: PAC1.0
DEVELOPMENTAL STAGE: N/A
                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: Linear
MOLECULE TYPE: Plasmid DNA
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IMMEDIATE SOURCE: N/A POSITION IN GENOME: N/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             / Match
Local Similarity 69.1%;
hes 38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 5595
TYPE: NUCLEIC ACID
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HAPLOTYPE: N/A
TISSUE TYPE: N/P
CELL TYPE: N/A
CELL LINE: N/A
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Gaps

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Matches

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Search completed: Wed Sep 15 10:38:57 1999 Job time : 19 secs.
 OPERATING SYSTEM:
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Sequence 5, Application US/08238163
Sequence 5, Application US/08238163
Sequence 5, Application US/08238163
Sequence 5, Application US/08238163
GENERAL INFORMATION:
APPLICANT: BENNETT, Alan
APPLICANT: BOWELL, Ann M.
APPLICANT: STOTZ, Henrik
TITLE OF INVENTION: PLANT INHIBITORS OF FUNGAL
TITLE OF INVENTION: POLYGALACTURONASES AND THEIR USE TO CONTROL FUNGAL DISEASE
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
IIILE OF INVENTION: POLYGALACTURONASES AND THEIR USE TO CONTROL FUNGAL DISEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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LOCATION: 1..215
OTHER INFORMATION: /standard_name= "Deduced amino acid
OTHER INFORMATION: sequence of PGIP from bean."
SEQUENCE 215 BP; 15 A; 8 C; 25 G; 26 T; 141 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match 17.5%; Score 20; DB 1; Length 215; Best Local Similarity 22.9%; Pred. No. 2.71e+00; Matches 8; Conservative 17; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SSEE: Townsend and Townsend Khourie and Crew 1: Steuart Street Tower, One Market Plaza San Francisco
                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/238,163
FILING DATE: 03-MAY-1994
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Revin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 2307E-540
TELECOMMUNICATION INFORMATION:
                                  ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: Steuart Street Tower, One Market Plaza CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               132 RIGKTANNAVDSRNMGDASVGSDKNTKKHAKNSAD 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JT 15
US-08-238-163-5 STANDARD; DNA; UNC; 215 BP.
                                                                                       COUNTRY: US
ZIE: 94105-1493
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 94105-1493
COMPUTER REACABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                        TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 215 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: unknown
MOLECULE TYPE: protein
             NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: California COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
LOCATION: 1..215
OTHER INFORMATION: /standard_name= "Deduced amino acid
OTHER INFORMATION: sequence of PGIP from bean."
SEQUENCE 215 BP; 15 A; 8 C; 25 G; 26 T; 141 OTHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 17.5%; Score 20; DB 1; Length 215; Best Local Similarity 16.1%; Pred. No. 2.71e+00; Matches 9; Conservative 26; Mismatches 21; Indels
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/238,163
FILING DATE: 03-MAY-1994
CLASSIFICATION: 800
ATTONEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 2307E-540
TELEPHONE: (415) 543-9600
TELEPHONE: (415) 543-5043
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 215 base pairs
TYPE: nucleic acid
STRNDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                unknown
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~ Wed Sep 15 12:54:07 1999

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n.a. - n.a. database search, using Smith-Waterman algorithm MPsrch\_nn

Wed Sep 15 10:47:40 1999; MasPar time 268.21 Seconds 995.949 Million cell updates/sec Run on:

Tabular output not generated.

>US-09-068-507A-2 (1-114) from US09068507A.seq 114 Title: Description: Perfect Score: N.A. Sequence: Comp:

1 ATGATGATATTTAAAAACT .........AAATTTTTACCCATGGTAA 114 TACTACTATAAAATTTTTTGA......TTTAAAAATGGGTAGCAATT

TABLE default Gap 6 Scoring table:

2883791 seqs, 1171580779 bases x 2 Searched:

Dbase 0; Query 0

Nmatch STD

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

Database:

embl-est58
1:em\_est10 2:em\_est11 3:em\_est17 4:em\_est18 5:em\_est2
6:em\_est9 7:em\_gss1
genbank-est11
8:pb\_est10 10:pb\_est11 11:gb\_est12 12:gb\_est13
13:qb\_est14 14:gb\_est15 15:gb\_est16 16:gb\_est17
13:qb\_est18 18:gb\_est19 19:gb\_est2 20:gb\_est20
21:gb\_est21 22:gb\_est22 23:gb\_est2 20:gb\_est24
25:gb\_est25 26:gb\_est26 27:gb\_est2 28:gb\_est28
25:gb\_est28 36:gb\_est2 31:gb\_est4 32:gb\_est5 33:gb\_est6
34:gb\_est7 35:gb\_est8 36:gb\_est9 37:gb\_gss1 38:gb\_est6
39:gb\_est7 35:gb\_est8 41:gb\_gss5 42:gb\_gss6

Mean 9.510; Variance 3.329; scale 2.857 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

		Pred. No.		3.536-08	2.71e-07	1.97e-06	4.01e-03	4.01e-03	4.01e-03	2.45e-02	2.45e-02	2.45e-02	2.45e-02
		Description P		3/SNI/0/ RICE IMMACUIE	AF034173 Human mRNA (T	97SN1787 Rice Immature	aq47e06.xl Stanlev Fro	aq46e06.xl Stanley Fro	CDG0587A CDIOWAGDNA1 C	RPCIII-69M19.TJ RPCIII	vv45d06.rl Soares 2NbM	AU039222 Dictyostelium	RPCI11-74G21.TJ RPCI11
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		DB		4	50	17	24	24	39	40	18	25	40
æ	Query	Length	253		2275	252	365	392	675	356	359	423	434
		Match	27.2	7.	26.3	25.4	21.9	21.9	21.9	21.1	21.1	21.1	21.1
		Score		1	30	59	25	25	25	24	24	24	24
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74 AU033574 Dictyostellum 2.45e- 75 Co24937 XI NCL_GAP_UT 1.44e- 77 MCE3650 XI NCL_GAP_UT 1.44e- 88 EST38687 Embryo, 9 wee 1.44e- 87 GS929 Yuli Kohara unp 1.44e- 87 CEKKO21HYR Yuli Kohara 1.44e- 78 Ox31e12. SI Soares_tota 1.44e- 79 Ox31e12. SI Soares_tota 1.44e- 85 EST3833 Parathyroid 9 1.44e- 86 EST83933 Parathyroid 9 1.44e- 87 CIT-HSP-386F22 TR CIT- 1.44e- 87 J\$9905. SI Soares brea 1.44e- 87 HOMGS01040 Human promy 1.44e- 87 HOMGS01040 Human promy 1.44e- 88 CELKO1069R Yuli Kohara 1.44e- 88 CS97718 DICTYOSTELIUM 0 1.44e- 88 CS97718 DICTYOSTELIUM 0 1.44e- 89 TENUZ540 T. CITZI EPIM 0 1.44e-	25.218 B 10.519.52 LT. B 2.11.	mRNA  eed Lambda ZAPII cDNA Library Oryza sativa leed Lambda ZAPII cDNA Library Oryza sativa la sequence.  Streptophyta; Embryophyta; Tracheophyta; phyta; Magnollophyta; Liliopsida; Poales; ong,J.J., Kim,S.I., Hahn,T.R. Moon,E.P., 'M.S., Park,R.D., Sohn,U.I., Kang,K.Y., nalysis of ESTs from Rice Immature Seed luence version replaced gi:1797457.	i. and Tech, RDA i.kr v. Dept of Biological Science, Myongji 449-728 bhnahm@bloserver.myongji.ac.kr imer. sativa"
AU033 A0344 A0344 A0399 A0399 C5992 D3281 A0371 A0371 A0371 A0371 C92712 C92712	CONTROL OF CONTROL OF	ALIC Ire S mRN 165 Chematc	un M.Y. of Cytogenetics ngst. of Agri. Sci. nggido, Korea 1 290 0301 1 290 0307 1 290 0307 by Back Hie Nahm, ly Back Hie Nahm, ly Yongin, Korea. 4 .: M13 Reverse Primm Cocation/Qualifiers organism="Oryza sa:
20 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 4 0 4 0 4 0 0 0 0 0 0 0 0 0 0 0	AA754459 252 bg 978M1787 Rice Immatucons clone 978N1787 AA754459.1 GI:2801165 AA754459.1 GI:2801165 AA754459.1 GI:2801165Tr Oryza sativa. Oryza sativa. Oryza sativa. Oryza sativa. Oryza sativa. Oryza sativa. Oryza sativa. Oryza sativa. Oryza sativa. Oryza sativa. Oryza sativa. Oryza sativa. Oryza sativa. Oryza sativa. Oryza sativa. Oryza sativa. Oryza sativa. Oryza sativa. Oryza. Oryza. I doses. I to 252) I doses. I to 252) I doses. I to 252) I doses. I to 252) I doses. I to 252) I doses. I to 252) I doses. I to 1939 I dosesi dos dosesi dos dosesi dosesi dos dosesi dos dosesi dos dosesi dos dosesi dos dosesi dos dos dosesi dos dos dosesi dos dos dosesi dos dos dos dos dos dos dos dos dos dos	Eun M.Y.  of Cytc  Inst. of  Cytg  1031 290 03  131 290 03  131 290 03  131 290 03  131 290 03  131 290 03  131 290 03  131 290 03  131 290 03  131 290 03  131 290 03  131 290 03  131 290 03  131 290 03  131 290 03  131 290 03  131 290 03
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000 00 0 0 0	000 00 00 0000	SKVNA DLVR SKVNA DLVR	

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/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2: XhOI: Directional cDNA library inserted into lambda ZAPII vector at 5'end with EcoRI and 3' end with Xho I site." /db_xref="taxon:4530"
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/dev_stage="5 days after pollination"
/lab_host="E. coli SOLR"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AF034173 2275 bp mRNA EST 30-MAR-1998 AF034173 Human mRNA (Tripodis and Ragoussis) Homo sapiens cDNA clone ntcon2 contig, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                              58 VNWSTMTWGTVNWBNVSGDWHYWBVBNTKVDVGNHTRCSRWRBVTRMAHYHDYTNCBBYN 117
                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
Eukaryota, Matazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2275)
Triphodis,v. and Ragoussis,v.
Triphodis,v. and Ragoussis,v.
Generation of a transcription map in the region immediately centromeric to human MHC across the 6p21.2-6p21.3 chromosomal
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619 c 470 q 599 t 149 others
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Division of Medical and Molecular Genetics
Guys Hospiral
Tth floor, Guy's Tower, London SEl 9RT, UK
Email: nikos@nki.ni.
Location/Qualifiers
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Pred. No. 3.63e-08;
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/db_xref-"taxon:9606"
/map-"6p21.3"
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/cultivar="Milyang23"
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larity 9.5%;
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                                                                                                    /map-"6"
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Oryza sativa
Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta;
euphyllophytes: Spermatophyta: Magnollophyta: Liliopsida: Poales;
                  AA754459 252 bp mRNA EST 20-JAN-1998
97SN1187 Rice Immature Seed Lambda ZAPII cDNA Library Oryza sativa
cDNA Clone 97SN1787, mRNA sequence.
AA754459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /cultivar-"Milyang23"
/note-"Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
XhoI; Directional cDMa library inserted into lambda ZAPII
vector at 5 end with EcoRI and 3' end with Xho I site."
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/tissue_type="Immature Seed"
/dev_stage="5 days after pollination"
/lab_host="E. coli SOLR"
21 c 12 g 35 t 179 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Department of Cytogenetics
National Inst. of Agri. Sci. and Tech, RDA
Suwon, Kyunggido, Korea
Tel: 82 331 290 0301
Fax: 82 331 290 0307
Fax: 82 311 290 0307
Small: myeun@sun20.asti.re.kr
Submitted by Baek Hie Nahm, Dept of Biological Science, Myongji
University, Yongin, Korea. 449-728 bhnahm@bioserver.myongji.ac.kr
Seq primer: MI3 Reverse Primer.
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                                                                                                                                                                                                                                                                    Poaceae; Oryza.
1 (bases 1 to 252)
Nahm,B.H., Kim,J.K., Cheong,J.J., Kim,S.I., Hahn,T.R, Moon,B.P.,
Kim,W.T., Kim,W.Y., Yang,M.S., Park,R.D., Sohn,U.I., Kang,K.Y.,
                                                                                                                                                                                                                                                                                                                                                        Lee,M.C. and Eun,M.Y.
Large-scale Sequencing Analysis of ESTs from Rice Immature Seed
Unpublished (1998)
On Jan 14, 1998 this sequence version replaced gi:1797457.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 GATGATATTTAAAAAACTTTCAGAAAAAGAATTGCAAAAAATAAACGGTGGTATGGCAGG 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16 BAMMITSYBCHGNBVWVCVASHGNYMSVHNCIBRGIHCDCKNVNWSIMIWGIVNWBNVSG 75
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Pred. No. 1.97e-06;
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ilarity 12.7%;
Conservative
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                                                                                                                                                                              Oryza sativa.
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Wed:Sep 15 12:54:07 1999

TITLE JOURNAL COMMENT

FEATURES

REFERENCE AUTHORS

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/organishm= name saptens:
//orde="Organ: brain; Vector: pCR2.1-TOPO (Invitrogen);
Site_1: EcoRI; Total RNA (purified with Trizol and DNAsed before use) was reverse transcribed using a modified oligo-dr primer containing RsaI and HindIII sites.
Double- stranded cDNA was digested with RsaI, resulting in blunt ended cDNA of an average 0.1-2 kb in length.
Digested cDNA was split into two sets, one used as is say the driver, the other set was split in half again and each half linked to a different adaptor.
(5'-TCGACGGCGCGCGCGCAGT-3'), to be used as tester.
Subtraction was performed using the Clontech PCR Select CDNA subtraction kit. Pool of two mentally normal males, ages 41 and 53 (S-114, S-141) subtracted by pool of two bipolar males, ages 45 and 50 (S-111, S-128). Tissues were obtained from the Stanley Neuropathology Consortium (www.stanleylab.org). Library constructed and subtracted by Dr. Nancy Johnston [(410) 614-3918, day subtracted and subtracted and subtracted of two medial taxon: 9606"
//mp="6: 21g" | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 2007 | 20
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CpG0587A CpIOWAgDNAl Cryptosporidium parvum genomic, genomic survey
sequence.
AQ083705
1 (bases 1 to 392)
Hiller, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Krizman, D., Kucaba, T., Ledy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schallenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R. Wash J. NCI human EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -40UP from Gibco High quality sequence stop: 378.
                                                                                                                                                                                                                                                       Unpublished (1997)
On Jan 19, 1998 this sequence version replaced gi:2150725.
                                                                                                                                                                                                                                                                                                                                                                             Contact: Wilson RK
Washington University School of Medicine
4444 Porest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cryptosporidium parvum
Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
Cryptosporidiidae; Cryptosporidium.
1 (bases 1 to 675)
Strong, W.B. and Nelson, R.G.
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/tissue_type="frontal lobe (see description)"
/lab.host="NHOB (phage-resistant)"
58 c 77 g 119 t
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/organism="Homo sapiens"
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Local Similarity 79.1%;
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                          Eutheria: Primates: Catarrhin; Hominidae; Homo.

(bases 1 to 365)

Hiller, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S. Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Theistin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theisting, B., White, Y., Wylle, T., Waterston, R. and Wilson, R. Unpublished (1997)
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla;
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aq46e06.xl Stanley Frontal NB pool 2 Homo sapiens cDNA clone
IMAGE:2033986, mRNA sequence.
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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/clone_lib="Stanley Frontal NB pool 2"
/tissue_type="frontal lobe (see description)"
/lab_host="DH10B (phage-resistant)"
/ 3 9 106 t
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Pred. No. 4.01e-03;
0; Mismatches 9;
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/organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: est@watson.wustl.edu
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Best Local Similarity 79.1%;
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 314 286 1800
Fax: 314 286 1810
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1 (bases 1 to 356)

3 Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P. and Venter, J.C. Use of human BAC End Sequences for Sequence-Ready Map Building Unpublished (1998)

1 Unpublished (1998)

2 Contact: Mark Adams

2 Contact: Mark Adams

3 Contact: Mark Adams

4 Department of Eukaryotic Genomics

7 The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

7 Tel: 301 838 0208

Fax: 301,838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AQ268382 356 bp DNA GSS 26-OCT-1998
RPCIll-69M19.TJ RPCIll Homo sapiens genomic clone R-69M19, genomic
survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (http://sequence-
www.stanford.edu/group/techdev/shear.htm). The randomly
sheared gDNA was chromatographed on Sephacryl S-400 to
remove any small fragments and DNA eluting in the void
volume was subcloned into an EcoR V-digested, alkaline
phosphatase-treated pBlueScript II (SK-) vector and
transformed into E. coll strain XL2 Blue MRF'.
Recombinant clones from the first plating of the library
were selected for sequence analysis using T3 and T7
                                                                                                                                                                                                                                                                                                                                                                                           /note="Vector: pBlueScript II (SK-); Site_1: EcoRV; C. parvum (IOWA isolate) genomic DNA was hydrodynamically sheared to produce fragments having a tight size distribution between 2-4 kb by Dr. Yoonne Thorstenson of the Stanford DNA Sequencing and Technology Center
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                   Contact: Nelson, R. G.
Depts. of Medicine & Pharmaceutical Chemistry
San Francisco General Hospital-University of California, San
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For clone availability, please contact Pieter de Jong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 25; DB 39; Length 675; Pred. No. 4.01e-03; 0; Mismatches 2; Indels
                                                                                                                                      Francisco
Box 0811, San Francisco, CA 94143-0811, USA
Tel: 415 206 8846
Fax: 415 206 3353
Email: malaria@itsa.ucsf.edu
Seq primer: M13(-21) forward
                                                                                                                                                                                                                                                                                                                                                  /organism="Cryptosporidium parvum"/strain="IOWA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="Cprowagbnal"
/lab_host="E. coli XL2 Blue MRF'"
93 c 95 g 216 t
Cryptosporidium parvum GST Project Unpublished (1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 21.9%;
Best Local Similarity 93.1%;
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                        1. .675
                                                                                                                                                                                                                                                                                    Class: shotgun.
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  TITLE
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AUTHORS
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JOURNAL
COMMENT
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                                                                                                                                                                                                                                                                                                         FEATURES
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                                                COMMENT
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Muscula;
Eutheria; Rodentia; Sclurognathi; Muridae; Muscula; Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Musca, Mus
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Clones may be purchased from Research Genetics (info@resgen.com). BAC end search page:
ttp://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: SP6
Class: BAC ends.
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vv54066.rl Soares 2NbWT Mus musculus cDNA clone IMAGE:1225355 5',
mRNA sequence.
AA764146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; RPCIII Human Male BAC Library"
/db_xref="GDB:7526418"
/db_xref="taxon:9606"
/clone="R-69M19"
/clone="R-69M19"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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On Apr 14, 1993 this sequence version replaced g1:693044.
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Tel: 314 286 1800
Fax: 314 286 1810
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Pred. No. 2.45e-02;
0; Mismatches 11; Indels
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Washington University School of MedicineP
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Seg primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 339.
Location/Qualifiers
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    .359
    /organism="Mus musculus"

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1.356
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /cell_type="Lymphocytes'
62 c 45 g 13
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AA764146.1 GI:2811668
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 21.1%;
Best Local Similarity 76.1%;
Matches 35; Conservative
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AQ268460 434 bp DNA GSS 26-OCT-1998
RPCIll-74G21.TJ RPCIll Homo sapiens genomic clone R-74G21, genomic
                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 434)

Adams, M.D., Rounaley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P. and Venter, J.C. Use of human BAC End Sequences for Sequence-Ready Map Building Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: mdadams@tigr.org
for clone availability, please contact Pieter de Jong
(pieter@dejong,med.buffalo.edu). Clones may be purchased from
Research Genetics (info@tesgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: SF6
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AU033574 435 bp mRNA along mRNA hara) Dictyostelium discoideum SL (H.Urushihara) Dictyostelium discoideum cDNA clone SLB183, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCIII Human Male BAC Library"
/db_xref="CBB:7528196"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
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Dictyostellum discoideum
Ekaryota, Dictyostellida; Dictyostellum.
1 (bases 1 to 435)
Yoshino,R., Morio,T. and Tanaka,Y.
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74 c 89 g 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="R-74G21"
/clone_lib="RPCI11"
/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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                                                                                                                                AQ268460.1 GI:3796064
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llarity 76.1%;
Conservative
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                                                              survey sequence.
                                                                                                                                                                                                   Homo saptens
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nes 35; Conser
                                                                                  A0268460
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                                 DEFINITION
                                                                                                                                                                                                 ORGANISM
                                                                                                                                                                                                                                                                                                                                    TITLE
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(Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. RNA provided by Dr. Bertrand Jordan. Library went through two rounds of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo."
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(bases 1 to 423)
Morio,T., Urushinara,H., Saito,T., Ugawa,Y., Mizuno,H., Yoshida,M., Yoshino,R., Mitra,B.N., Pi,M., Sato,T., Takenoto,K., Yasukawa,H., Williams,J., Maeda,M., Takeuchi,I., Ochiai,H. and Tanaka,Y.

The Dictyostelium developmental cDNA project: generation and analysis of expressed sequence tags from the first-finger stage of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AU039222 423 bp mRNA EST 29-MAR-1999
AU039222 Dictyostelium discoideum SL (H.Urushihara) Dictyostelium
discoideum cDNA clone SLH180, mRNA sequence.
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/clone_lib="Dictyostelium discoideum SL (H.Urushihara)"
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Email: d402hu@sakura.cc.tsukuba.ac.jp
PROJECT = 'Dictyostelium discoldeum cDNA project in Japan'
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                                                                                                                                         /clone="IMAGE:1225355"
/clone_lib="Soares 2NbMT"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Hideko Urushihara
Institute of Biological Sciences
University of Tsukuba
                                                                                                                                                                                                      /tissue_type="Thymus"
/dev_stage="4 weeks"
/lab_host="DH10B"
a 56 c 65 g
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/db_xref="taxon:44689"
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99156227
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57 c 44 g
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Best Local Similarity 71.4%;
Matches 40; Conservative
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21.1%;
Best Local Similarity 76.1%;
Matches 35; Conservative
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RESULT

셤 ŏ DEFINITION

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REFERENCE AUTHORS

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Length 434;

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On Jan 14, 1998 this sequence version replaced gi:1798828
                                                           Contact: Hideko Urushihara
Institute of Biological Sciences
University of Tsukuba
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328 TATTGTCTGCAATTCTTTGAATGAAAGTTTTTTA 361
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Building
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For clone availability, please contact Pieter de Jong

For clone availability, please contact Pieter de Jong

For clones may be purchased from

Research Genetics (info@resgen.com). BAC end search page:

http://www.tigr.org/tdb/humgen/bac_end_search.html.

Seq primer: SP6
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                                                                                                                                               /clone_lib="Dictyostelium discoldeum SL (H.Urushihara)"
/dev_stage="slug"
62 c 43 g 148 t
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Adb Arzef="GDB:7543600"

Adb_Arzef="taxon:9606"
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Eukaryota: Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Prinates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 530)
2 Abao, S., Adams, M.D., Nierman, W., Malek, J., de Jong, P. and Venter, J.C.
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RPCII1-114117.TJ RPCII1 Homo sapiens genomic clone R-114117,
                                                                                                                                                                                                                                                                                                     Email: d402hu@sakura.cc.tsukuba.ac.jp
PROJECT - Dictyostelium discoideum cDNA project in Japan.
Location/Qualifiers
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Other_GSSs: RPCIII-114II7.TV
Other_GSSs: RPCIII-114II7.TV
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Fax: 301 838 0208
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Pred. No. 2.45e-02;
 3-3-10 Ten-nodai, Tsukuba, Ibaraki 305, Japan
                                                                                 /organism-"Dictyostelium discoideum'
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67 c 108 g 13
                                                                                                 /strain="Ax4"
/db_xref="taxon:44689"
/clone="SLB183"
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1. .530
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/clone_lib="RPC111"
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ilarity 71.4%;
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ilarity 85.3%;
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Tal: (301) 496-1550
Email: Robert_Strausberg@n.h.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Ph.D., Ph.D., Ph.D., Ph.D., Ph.D., Ph.D., DNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-GGAP clone distribution information can be found through the I.M.A.G.E., Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.85 kb. Life Technologies catalog #:
11539-012"
                                                                                                                                                  AI570972 133 bp mRNA EST 29-MAR-1999 to24q03.x1 NCI_CGAP_Ut2 Homo sapiens cDNA clone IMAGE:2180020 3' similar to contains element LTR3 repetitive element ; mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalla;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 133)
NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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WCCES560.MIF Schistosoma mansoni, cercariae Schistosoma mansoni
CDNA clone SM3650C 3' end, mRNA sequence.
AA999637
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/clone="IMAGE:2180020"
/clone=lib="NCI_CGAP_Ut2"
/closue_type="moderately-differentiated endometrial
denocarcinoma, 3 pooled tumors"
/lab_host="DH10B"
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Unpublished (1997)
On Mar 20, 1998 this sequence version replaced g1:2980227
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45 TATTTTTGCAATTCTTTTTCTGAAAGTTTTTTA 12
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High quality sequence stop: 103.
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Schistosoma mansoni.
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Best Local Similarity
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. Wed.Sep 15 12:54:07 1999

Schistosoma mansoni

ORGANISM

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234 ATAAAATTTAAAAATTTAAAAAAAAAGGTTTGCAAAATGTAA 276
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Eukheria; Primates; Catarrhin; Hominidae; Homo.

Eutheria; Primates; Catarrhin; Hominidae; Homo.

1 (bases 1 to 293)

Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldher, R.A., Milte, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Bardon, R.C., Man'Wall, C., Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S.Jr., Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shriey, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A.,
Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma. [ tbases 1 to 252)
Santos, T. M., Azevedo, V., Marotta, G.B., Santos, R.L., Fonseca, S.J., Ortega, J.M., Rabelo, E.M.L., Saber, M., Abdel-Hamid, H., Ridgers, I.L., Johnston, D.A., Fernandez, M., Rollinson, D., Franco, G.R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Avenida Antonio Carlos 6627, Belo Horizonte, MG, Brazil, 31270-010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Schistosoma mansoni"
/strain="NNRI"
/strain="NNRI"
/note="Vector: pBlueScript SK; Site_1: XhoI; Site_2:
BCORI; mRNA was extracted from cercariae and the library
was constructed and excised according to the
manufacturer and excised according to the
Stratagene)"
Stratagene)"
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                                                                                                                                                                                                                                                                                                                                                                                       Laboratorio de Genetica-Bioquimica, Departamento de Bioquimica e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA334468 293 bp mRNA EST 21-APR-1997
EST38687 Embryo, 9 week Homo sapiens cDNA 5' end, mRNA sequence.
AA334468
                                                                                                                                                                                                                                                                                                                                                                                                                                             Instituto de Ciencias Biologicas, Universidade Federal de Minas
                                                                                                                                                                                                Analysis of the Gene expression profile in Schistosoma manson
cercariae using EST approach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 23; DB 21; Length 252;
Pred. No. 1.44e-01;
0; Mismatches 15; Indels 0; Gaps
                                                                                                                                                                                                                                                                Unpublished (1998)
On Jan 17, 1998 this sequence version replaced gi:2043380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="Schistosoma mansoni, cercariae"
                                                                                                                                                                                                                                                                                                                                                           Contact: Santos, T.M. and Pena, S.D.J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: (5531)4415611
Fax: (5531)4415409
Email: santostm@mono.icb.ufmg.br
Seq primer: M13 Forward.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:6183"
/clone="SM3650C"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /dev_stage="Larvae"
/lab_host="DH5alpha"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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Best Local Similarity 71.7%;
Matches 38; Conservative
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                                                                                                                                                                                                                                                                JOURNAL
                                                            REFERENCE
                                                                                        AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KEYWORDS
SOURCE
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                                                                                                                                                                                                            TITLE
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He,W.W., Hu,J.S., Greene,J.W., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Melssner,P.S., Olsen,H., Raymond,L., Wei,Y.F., Wingy,J., Xu,C., Yu,G.L., Ruben,S.M., Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.

Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
Information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                    On Apr 14, 1993 this sequence version replaced gi:716849. Other_ESTS: THC178342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                                                                                                                                                                                     9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="Embryo, 9 week"
/dev_stage="embryo, 9 wks"
/dev_stage="embryo, 9 wks"
51 c 46 g 116 t
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The Institute for Genomic Research
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/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                  Contact: Kerlavage, AR
                                                                                                                                                                                                                                            96026280
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Search completed: Wed Sep 15 10:52:51 1999 Job time: 311 secs.

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